Master's Thesis

Proteomic analysis of organelle-contact sites using a split, promiscuous biotin ligase in live cells

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Abstract

Organelle-contact sites are crucial for organelle communications and regulating homeostasis. Although growing interest exists for understanding resident proteins at contact sites, conventional methods are limited. Herein, we present a novel proteomic mapping method of the local proteome at an organelle-contact site, based on a split, promiscuous biotin ligase (pBirA). After screening for temporal biotinylated activities, we selected split pBirA system which divided into N-G78 and G79-C, which showed strong biotinylated activities only when complexed. We named this system as MCS-ID and targeted this to the endoplasmic reticulum (ER) membrane and outer mitochondrial membrane (OMM), respectively, in mammalian cells using anchoring transmembrane proteins and identified biotinylated proteins by mass spectrometry. We identified 72 proteins reproducibly labeled by MCS-ID, 69 of which were novel ER–OMM junction proteins. We also identified 14 proteins localizing to the ER–OMM junction during starvation. The major functions of these proteins were related to ubiquitination, which affect mitochondrial quality or mitophagy. Our new method (MCS-ID) facilitated reliable identification of the local proteome at the ER–OMM contact site, and it can potentially be employed to map other organelle-contact sites in live cells.

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List of Abbreviations

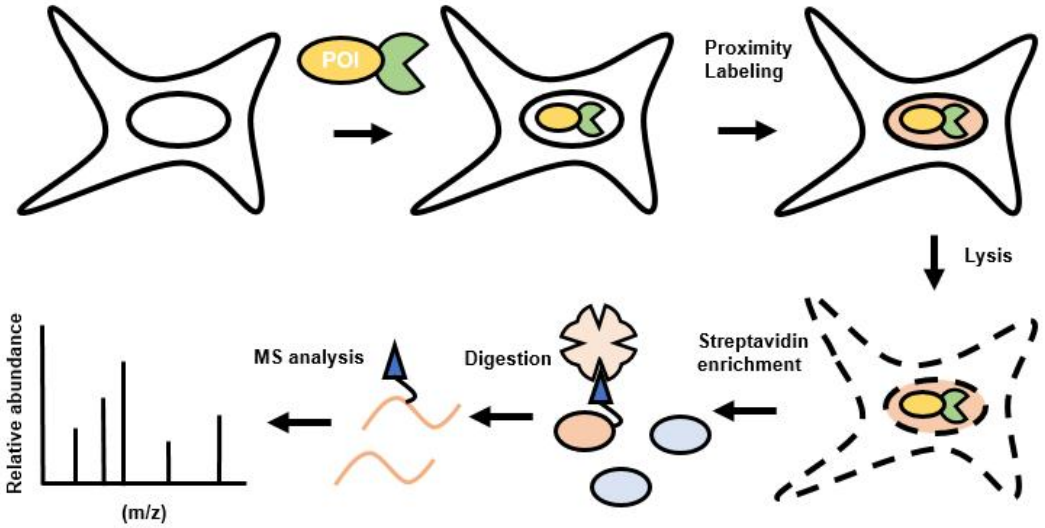
ABC	Ammonium bicarbonate
AD	Alzheimer's disease
ALS	Amyotrophic lateral sclerosis
AMP	Adenosine monophosphate
APEX	Engineered ascorbate peroxidase
CID	Collision-induced dissociation
CMT2A	Charcot Marie Tooth disease Type 2A
CMV	cytomegalovirus
DAB	diaminobenzidine
DPBS	Dulbecco's phosphate-buffered saline
DTT	Dithiothreitol
EDTA	Ethylenediaminetetraacetic acid
ER	Endoplasmic reticulum
ERM	ER cytosolic facing membrane
EF-TEM	Energy-filtered transmission electron microscopy
FBS	Fetal bovine serum
FDR	False discovery rate
FTD	Frontotemporal dementia
HA	Hemagglutinin
HPLC	High-performance liquid chromatography
HRP	Horse radish peroxidase
MCS	Membrane contact sites
MS	Mass spectrometry
m/z	Mass to charge
NCBI	National center for biotechnology information
OMM	Outer mitochondrial membrane
OsO_4	Osmium tetroxide
pBirA	Promiscuous biotin ligase
PBS	Phosphate-buffered saline
PCR	Polymerase chain reaction
PD	Parkinson's disease
PDB	Protein data bank
PMSF	Phenylmethylsulfonyl fluoride
PMT	Photo multiplier tube
PPI	Protein-protein interaction
PPM	Parts per million
PSM	Peptide spectrum match
RIPA	Radioimmunoprecipitation assay
TCEP	Triphosphine hydrochloride
TM	Transmembrane protein

. Introduction

1.1 Practical limitations of the conventional purification method and enzyme catalyzed proximity labeling in proteomic profiling

Many physiologically important processes occur in specific subcellular organelles or regions. In addition, the functions of proteins are related to their subcellular localizations and interactions between them. Thus, analyzing proteome located in specific organelles plays the important roles in understanding complex subcellular processes. However, conventional purification methods using pull down assays or crosslinking have many limitations. First, in many cases it is difficult to selectively fractionate certain subcellular organelles at high purity. Second, even if fractionation is possible, there is a risk of contamination causing false-positive identification. Third, it is difficult to reflect the state of living cells as the purification process proceeds in an artificial buffer.

For this reason, proximity labeling methods have recently been used in biological community to profiling proteome present in certain organelles. In general, proximity labeling method uses an enzyme conjugation with a targeting signal sequence or protein of interest. There are three major enzymes used here: promiscuous biotin ligase[1] (pBirA), horse radish peroxidase[2] (HRP) and ascorbate peroxidase[3] (APEX). After targeting these enzymes, enzyme catalyzed proximity labeling reaction is performed in living cell state. These labeled proteins are enriched by streptavidin beads and digested by trypsin. The processed peptides have a mass to charge (m/z) ratio, which is used to identify the peptide sequence (**Scheme 1**).



Scheme 1. General proximity labeling method for proteomic profiling.

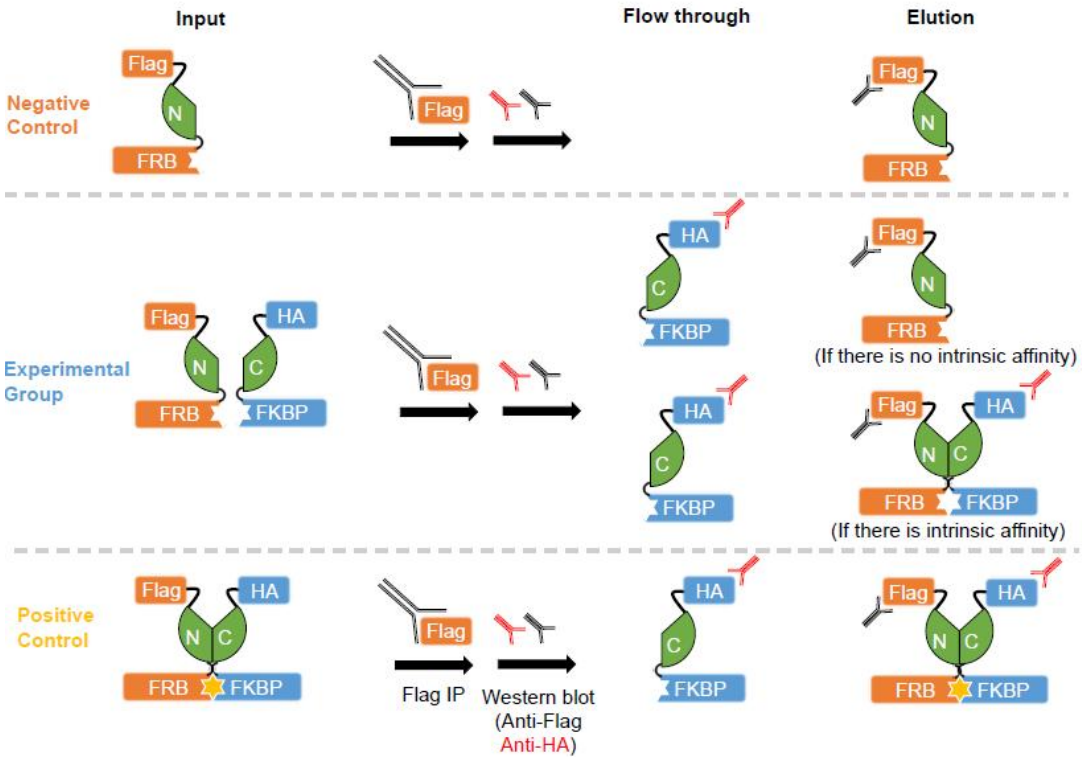
1.2 Limitations of proximity labeling method in membrane contact sites (MCS)

For MCS-localized proteome mapping studies, however, proximity labeling methods are not yet successful because no MCS-specific marker protein has been identified to date, as all characterized MCS proteins also co-localize with the either side of membrane[4-5]. Thus, the results obtained from this proximity-based labeling method cannot be regarded as the MCS proteome.

Therefore, an attempt to introduce a split system into an enzyme used for such proximity labeling has been actively conducted recently. Conceptually, this method involves conjugating two membrane targeting sequences to each fragments of bisected enzymes. Then, the split enzyme is reassembled in the MCS and the enzyme becomes active and labels the MCS proteome.

A way using split HRP[6] was first invented by Alice ting's group in 2016, however, it was not active in the reducing environments such as cytosol. Also because of intrinsic affinity between two split fragments, it was declared that it is not suitable for intracellular labeling.

Another attempt has been to split pBirAs on E140, Q141 amino acids[7] or on E256, G257 amino acids[8]. However, in these both of two cases, split pBirAs are not suitable for intracellular labeling. In former case, we observed that those split systems showed consistent biotinylating activity that was not controlled by rapamycin, implying that the biotinylating activity of these previously reported pairs may not be temporally controlled by the protein-protein interaction (PPI) of the conjugated proteins because of their high intrinsic affinities for each other. In later case, reassembly activity was not sufficient for MCS proteomic profiling (**Scheme 2**, **Figure 1**). Intrinsic affinity is due to the characteristic that the split enzyme is going to be the original assembly. These artificial element increases the membrane contact and thus affect the various metabolic activities induced by MCS.



Scheme 2. Schematic illustration of intrinsic affinity assay after immunoprecipitation for split systems.

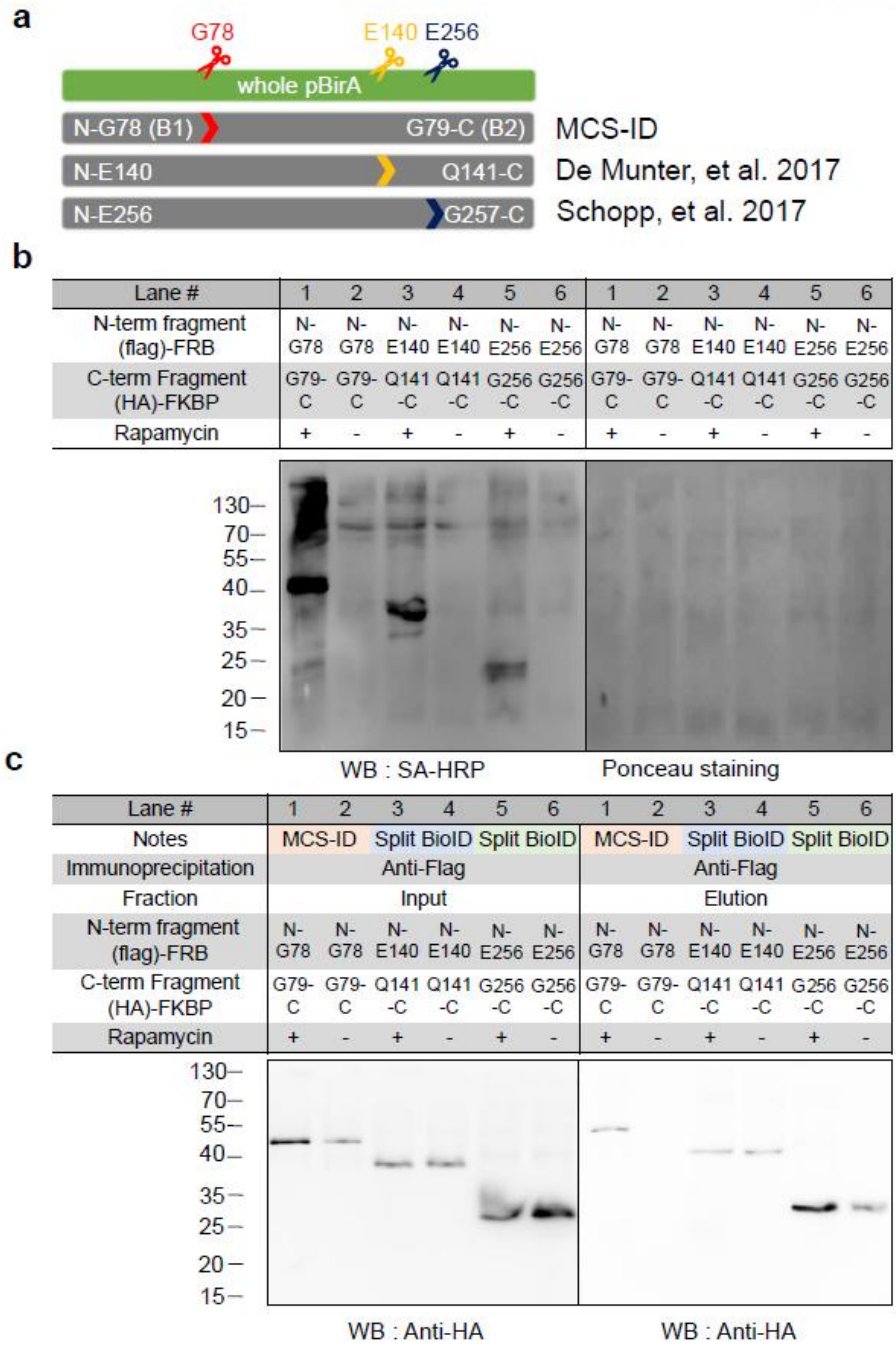


Figure 1. Comparison of intrinsic affinity of other split pBirA systems.

a. Construct of split pBirAs in use. Split pBirA in G78-G79 (as MCS-ID) was utilized in following all experiments. **b.** Comparison of activity for split pBirA systems in FKBP-FRB system. In presence of rapamycin, split pBirAs were reassembled by FKBP-FRB heterodimerization. Each N-terminus of FRB were conjugated with N-terminus split fragments. Each C-terminus of FKBP were conjugated with C-terminus split fragments. **c.** After immunoprecipitation using flag antibody as **Scheme 2**, intrinsic affinity assay results. Compared with other systems, G78-G79 showed no intrinsic affinity at all.

1.3 Physiological importance of MCS proteome

Organelles communicate with each other through organelle-contact sites[9-10]From recent advance of biological imaging techniques, more membrane contact sites (MCS) between cellular organelles have been identified and their functional roles has been recognized to regulate cellular homeostasis.[11] Among these MCSs, mitochondrial-associated ER membrane (MAM), which is a MCS between endoplasmic reticulum (ER) and mitochondria is known to regulate many physiological processes including calcium homeostasis[12], lipid transport[13], organelle biogenesis[14], regulating organelle stress[5], and cell cycle modulation.[15-16] Thus, this ER-mitochondria axis is recently recognized to cause several neurodegenerative diseases[17-18] such as Alzheimer's disease (AD), Parkinson's disease (PD), and amyotrophic lateral sclerosis with associated frontotemporal dementia (ALS/FTD) and Charcot Marie Tooth disease Type 2A (CMT2A). Recently, MAM is also recognized to be related to several metabolic diseases such as Type 2 Diabetes.[19-20] All these human diseases are related to abnormal functionality of MAM when one or several MAM proteins get a lethal mutation(s). Therefore, a distinct proteome at the organelle contact sites was identified and this local proteome has been recognized as containing biomarkers for a diverse spectrum of human diseases[16, 21-22].

However, the system for proper proteomic profiling has not been systematized for MCS where these physiologically important processes occur. Thus, we attempted to develop a novel split pBirA system which is suitable for mapping spatially-resolved residents at the MCS.

Ⅱ. Experimental Method & Materials

2.1 Plasmids and Cloning

Genes were cloned into the specified vectors using standard enzymatic restriction digest and ligation with T4 DNA ligase. To generate constructs where short tags (e.g., HA or Flag epitope tag) or signal sequences were appended to the protein, the tag was included in the primers used to PCR-amplify the gene. PCR products were digested with restriction enzymes and ligated into cut vectors (e.g., pcDNA3, and pDisplay). In all cases, the CMV promoter was used for expression in mammalian cells. **Table 1** below summarizes the genetic constructs cloned and used for this study.

Table 1. Plasmids Information.

Name	Features	Promotor/ Vector	Notes
FKBP-pBirA (Q65, G79, Q141, G257, S263, E284 -C)-HA	*NotI*-FKBP-*BamHI*-pBirA (Q65, G79, Q141, G257, S263, E284 -C)-HA-Stop-*XhoI*	CMV/ pCDNA3	pCDNA3.1 MCS-BirA(R118G)-HA was a gift from Kyle Roux (Addgene plasmid #36047) FKBP and FRB a gift from Takanari Inoue (Johns Hopkins University, Baltimore, MD)
Flag-pBirA (N-I64, G78, E140, E256, L262, K283)-FRB	*NotI*-FKBP-*BamHI*-pBirA (Q65, G79, E140, E256, S263, E284 -C)-HA-Stop-*XhoI*	CMV/ pCDNA3	
FKBP-An improved smaller pBirA (E132, K198-C)-HA	*NotI*-FKBP-*BamHI*-An improved smaller pBirA (E132, K198-C)-HA-Stop-*XhoI*	CMV/ pCDNA3	MCS-BioID2-HA was a gift from Kyle Roux (Addgene plasmid #74224)
Flag-An improved smaller pBirA (N-E131, G197)-FRB	*NotI*-FKBP-*BamHI*-An improved smaller pBirA (N-E131, G197)-HA-Stop-*XhoI*	CMV/ pCDNA3	
Flag-pBirA(N-G78, E256)-SEC61B	*NotI*-Flag-pBirA(N-G78, E256)-linker-*EcoRI*-SEC61B-Stop-*XhoI*	CMV/ pCDNA5	linker: GGASGGSGSGPVAT SEC61B (NM_006808)
TOM20-pBirA (G79, G257-C)-HA	*KpnI*-TOM20-*BamHI*-linker-pBirA (G79, G257-C)-HA-Stop-*NotI*	CMV/ pCDNA5	Linker: SGGSGGSR Tom20 (NM_014765.2)

UFD1L-mCherry	*KpnI*-UFD1L-*BamHI*-*NheI*-Flag-mCherry-Stop-*XhoI*	CMV/ pCDNA5	UFD1L-HA/Flag was a gift from J. Wade Harper
CYB5B-EGFP	ClaI-EBFP-KpnI-BamHI-NheI-Flag-NotI-CYB5B-Stop-AscI	CMV/ pCDNA5	CYB5B (NM 030579.2)
FKBP8-APEX2	*KpnI*-FKBP8-*BamHI*-V5-APEX2-Stop-*NotI*	CMV/ pCDNA5	FKBP8 (NM 012181.4) Mito-V5-APEX2 was a gift from Alice Ting (Addgene plasmid #72480)
APEX2-FKBP8	*HindIII*-APEX2-*KpnI*-V5-*NotI*-FKBP8-Stop-*AscI*	CMV/ pCDNA5	
Mito-APEX2	*KpnI*-Mito-*BamHI*-*NheI*-V5-APEX2-Stop-*NotI*	CMV/ pCDNA5	Mito-V5-APEX2 was a gift from Alice Ting (Addgene plasmid #72480)
SEC61B-APEX2	*NotI*-SEC61B-*NheI*-V5-APEX2-Stop-*XbaI*	CMV/ pCDNA3	

For subcellular localization marker, mito-BFP was a gift from Gia Voeltz (Addgene plasmid #49151) and EGFP-LC3 was a gift from Karla Kirkegaard (Addgene plasmid #11546). mApple-TOMM20-N-10 was a gift from Michael Davidson (Addgene plasmid #54955). mCherry and EBFP was amplified by PCR and subcloned into KDEL-pDisplay vector. SEC61B was amplified by PCR and subcloned into pEGFP vector.

2.2 Antibodies

Primary antibodies were used for western blotting and immunofluorescence imaging: Streptavidin, Alexa Fluor 647 conjugated (1:3000 dilution, Invitrogen, cat no. S-21374), Streptavidin, HRP conjugated (1:10000 dilution, Invitrogen, cat no. S-21126), Anti-Flag-mouse (1:3000 dilution, Sigma Aldrich, cat no. F3165), Anti-HA-rabbit (1:3000 dilution, Sigma Aldrich, cat no. H6908) Anti-PMP70-mouse (1:1000 dilution, Sigma Aldrich, cat no. SAB200181). Secondary antibodies including anti-mouse, rabbit-HRP and Alexa Fluor-conjugated anti-mouse, rabbit are purchased form Invitrogen.

2.3 Cell culture and transfection

HEK-293T cells from ATCC (Manassas, VA, USA) (passages < 20), COS-7 cells form the Korean Cell Line Bank were cultured in FBS-containing media. Cells were transiently transfected at 60–80% confluence using Lipofectamine 2000 (Life Technologies, Carlsbad, CA, USA). For starvation condition, cells were transferred into growing media without serum for 12 hours.

For generation of cells stably expressing MCS-ID, HEK-293T cell were transfected

at 60-80% confluence with Flag-pBirA(1-78)-SEC61B (in pLX304) and two lentiviral packaging plasmids (dR8.91 and pVSVG[23]) using Lipofectamine 2000. 48 hours after transfection, the cell culture media containing lentivirus was collected and filtered through a 0.45μm syringe filter. To a fresh HEK293T culture at ~70% confluence with ~200,000 cells was added 500 μL of the filtered lentivirus containing media. Two days after infection, cells were transferred to complete FBS media containing 2 μg/mL blasticidin for selection. Infected cells were maintained in 2 μg/mL blasticidin-containing media for 7 days (three passages). After generation of cells stably expressing Flag-pBirA(1-78)-SEC61B, next, HEK-293T cell were transfected cells with TOM20-pBirA(79-321)-HA and following viral infection was done in stably expressing Flag-pBirA(1-78)-SEC61B. Infected cell were selected until only cells having both constructs survived by colony picking. Validation process was done by immunofluorescence imaging with epitopes.

2.4 Fluorescence microscopy

Cells were plated on coverslips (thickness no. 1.5 and radius: 18mm). For live cell imaging, cells were transferred into growing media W/, W/O serum depending on experiments. For fixed cell imaging, cells were fixed by 4% paraformaldehyde and permeabilized with cold methanol for 5min at -20°C. Next, cells were washed with Dulbecco's phosphate-buffered saline (DPBS) and blocked for 1 h with 2% BSA in DPBS at room temperature. Immunolabeling was conducted in blocking solution with proper diluted antibodies.

Fluorescence microscopy imaging was performed on LSM 880 (IBS, Center for Genomic Integrity, Korea) and LSM780 (UOBC in UNIST, Korea) with alpha Plan-Apochromat 100x/ NA: 1.46 and PMT detectors, controlled by Zen software.

2.5 Electron microscopy

HEK293T cells were grown on 6-well cell culture plates. Cells were fixed on ice using cold 4% formaldehyde (Electron Microscopy Sciences, Hatfield, PA, USA) in PBS buffer for 15 min. All subsequent work was performed using pre-chilled buffers and reagents. Cells were again washed with PBS three times. Cells were permeabilized with 0.5% tween 20 (Sigma Aldrich) for 1 min and washed immediately with PBS for two times. Then, cells were blocked by blocking solution (2% dialyzed BSA in PBS) for 30 min and streptavidin in blocking solution was replaced after blocking. After 30 min incubation, Cells were washed by PBS six times each for 5 min. Cells were fixed on the ice by using 2% formaldehyde and 2% glutaraldehyde (Electron Microscopy Sciences) in PBS. Cells were kept on ice for all subsequent steps before dehydration steps. After 30–60 min, the cells were rinsed 5 × 2 min

each in chilled buffer and then treated for 5 min in buffer containing 20 mM glycine to quench the unreacted glutaraldehyde, followed by another 3 × 5 min rinses in chilled buffer. A freshly diluted solution of 1 mg/mL (2.8 mM) DAB free base was combined with 10 mM H_2O_2 in chilled buffer, and the solution was added to cells for 5 min. To halt the reaction, we removed the DAB solution and the cells were rinsed 3 × 5 min with chilled buffer. Post-fixation staining was performed using 2% (w/v) osmium tetroxide (Electron Microscopy Sciences) for 1 h in chilled buffer. Cells were rinsed 5 × 2 min each in chilled distilled water. Cells were brought to room temperature, washed in distilled water, and then carefully scraped off the plastic, resuspended, and centrifuged at 1600 ×*g* for 1 min to generate a cell pellet. The supernatant was removed and the pellet was dehydrated in a graded ethanol series (50%, 60%, 70%, 80%, 90%, 100%, 100%, 100%) for 15 min each time and solution was replaced with propylene oxide for 20 min; then, it was infiltrated into EMBED-812 (Electron Microscopy Sciences) using 1:1 (v/v) resin and anhydrous ethanol for 1 h. The second change of 2:1 (v/v) resin and anhydrous ethanol was incubated overnight. After removing the resin, the sample was exchanged once more with 100% resin for 2 h before transferring the sample to fresh resin, followed by polymerization at 60°C for 48 h. Embedded cell pellets were cut with a diamond knife into 50-nm sections and imaged on a EF-TEM in Korea Basic Science Institute in Chuncheon.

2.6 Immunoprecipitation analysis

For immunoprecipitation, cells were lysed with Cell Extraction buffer (Life technologies, FNN0011) containing 1× protease cocktail (Sigma Aldrich, catalog no. P8849), and 1 mM PMSF (phenylmethylsulfonyl fluoride) for 30 min at 4 ℃. Lysates were transferred to e-tube and vortexed for 2min. And lysates were clarified by centrifugation at 15,000g for 10 min at 4 °C.

Dynabeads Protein G (Invitrogen, 10003D) 40ul were incubated with 4ug of anti-flag-mouse during 30min at room temperature. The beads were washed two times using PBS with 0.1% tween20. Then cell lysates were incubated with Protein G beads during 1hr. The beads were washed three times using PBS with 0.1% tween20 and eluted by boiling at 95 °C for 10 min after 1x Laemmeli buffer with 1mM of DTT.

2.7 LC-MS/MS sampling and analysis

Cells were grown in two T75 flasks. Cells were transfected at 60–80% confluence. Addition of biotin 50uM was done after expression of constructs. the cells were washed three times with DPBS and then lysed with 1.5 mL RIPA lysis buffer (50 mM Tris, 150 mM NaCl, 0.1% SDS, 0.5% sodium deoxycholate, 1% Triton X-100), 1X protease cocktail (Sigma

Aldrich, catalog no. P8849), and 1 mM PMSF (phenylmethylsulfonyl fluoride) for 20 min at room temperature. After lysis of cells, all steps are done in room temperature or higher to prevent precipitation of detergents. Lysates were clarified by centrifugation at 16,000 × *g* for 10 min. To reduce lysates, TCEP (Triphosphine hydrochloride) was added in final conc. as 5mM and shook at 900 rpm for 60 min at 37 °C using a Thermomixer (Eppendorf). For concentrating and denaturation of lysates, we load the lysates on an Amicon filter (Merck Millipore, UFC801096) followed by centrifugation at 7500 × *g* for 20 min. 3ml of denaturing solution (8M urea in 50mM ammonium bicarbonate (ABC)) was added and centrifuged at 7500 × *g* for 20 min. Denaturation step was done additional and alkylation of protein was introduced by 3ml of denaturing solution containing 10mM Iodoacetamide without mixing for 30min under dark condition. After that, lysates are centrifuged at 7500 × *g* for 20 min and alkylation solution was added and centrifuged again with same condition. After alkylation steps, denaturation solution was added and centrifuged twice. To remove urea, last centrifugation was done with 1ml of 50mM ABC buffer and concentrated sample was transferred to 1.5ml of Eppendorf tube. Collection of remaining sample are followed with washing filter unit with 200ul of 50mM ABC buffer and final concentration of urea was adjusted under 200mM. For trypsinization, 1 mg/mL trypsin gold in acetic acid (Promega, V5280) was added in ratio of protein/ trypsin as 1:50). Sodium chloride (final conc. as 1mM) was added and incubated with shacking of 900rpm for overnight at 37 °C. To enrich labeled peptides, 150ul of streptavidin beads (Pierce) was mixed with digested peptide and incubated it 1hr with rotation. With three times of PBS washing, we removed non-specific binding peptides. 300ul of elution buffer (EDTA 10mM in formamide, pH8.2) was used and incubated at 95 °C for 10min.

2.8 Desalting

Varian Bond ELUT was activated with 1 mL of 3% acetonitrile/0.1% formic acid, 1 mL of 100% acetonitrile, and 2 mL of 3% acetonitrile/0.1% formic acid (v/v). Then, sample was added to column for binding (X2). The column was washed using 2 mL of 3% acetonitrile/0.1% formic acid (v/v). It was then eluted with 1.4 mL of 70% acetonitrile/0.1% formic acid (v/v) and 500 µL of 100% acetonitrile. The eluted fraction was dried in a speed-vac and kept in the refrigerator.

2.9 Mass spec detection of labeled peptide

All mass analyses were performed using an LTQ-Orbitrap mass spectrometer (Thermo, Bremen, Germany) equipped with a nanoelectrospray ion source. A C18 reverse-

phase HPLC column (150 mm x 75 μm i.d.) was used to separate the peptide mixture using a 10 to 24% acetonitrile/0.1% formic acid gradient for 90 min at a flow rate of 300 nL/min. For MS/MS analysis, precursor ion scan MS spectra (m/z 400~2000) were acquired using the Orbitrap spectrometer at a resolution of 60,000 at 400 m/z with an internal lock mass. The 20 most intensive ions were isolated and fragmented in the linear ion trap by collision-induced dissociation (CID).

2.10 MS Data Processing

MS/MS spectra were analyzed using the following data processing protocol.

Database searching—All MS/MS samples were analyzed using Sequest (Thermo Fisher Scientific, San Jose, CA, USA; version 1.4.1.14) and X! Tandem (The GPM, thegpm.org; version CYCLONE (2010.12.01.1)). Sequest and X! Tandem were set up to search the *Homo sapiens* protein sequence database (89113 entries, UniProt (http://www.uniprot.org/)) assuming digestion with the enzyme trypsin. Sequest and X! Tandem were searched with a fragment ion mass tolerance of 0.60 Da and a parent ion tolerance of 10.0 PPM. Carbamidomethyl cysteine was specified in Sequest and X! Tandem as a fixed modification. The following conditions were used: Glu->pyro-Glu of the n-terminus, ammonia-loss of the n-terminus, gln->pyro-Glu of the n-terminus, oxidation of methionine and biotin of lysine were used in X! Tandem and Sequest as variable modifications.

Criteria for protein identification—Scaffold (version Scaffold_4.5.1, Proteome Software Inc., Portland, OR) was used to validate the MS/MS-based peptide and protein identifications. Peptide identifications were accepted if they could be established at greater than 84.0% probability to achieve an FDR less than 1.0% by the Scaffold Local FDR algorithm. Protein identifications were accepted if they could be established at greater than 90.0% probability to achieve an FDR less than 1.0% and contained at least one identified biotin labeled-peptide. Protein probabilities were assigned using the Protein Prophet algorithm (Nesvizhskii, Al et al Anal. Chem. 2003;75(17):4646-58). Proteins that contained similar peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony. Proteins were annotated with GO terms from the NCBI database (downloaded Jan 22, 2016) (Ashburner, M et al Nat. Genet. 2000;25(1):25-9).

2.11 Image analysis

Images were digitally processed as follows. A rolling-background subtraction with a width of 8 pixels was applied to improve the signal-to-noise ratio in the fluorescence images. The distance between the center of UFD1L-mCherry and the surface of the MAM was measured manually.

2.12 Molecular dynamics simulation analysis

To estimate the degree of free movement within the structure of proteins, we got the B-factor data from the Protein Data Bank (PDB). B-factor (also known as temperature factor or Debye-Waller factor) are used to describe the attenuation of X-ray scattering[24]. Generally, B-factor of less than 30$Å^2$ is considered to signify confidence in its positions and greater than 60 $Å^2$ is considered to signify disorder. We used previously reported crystal structure of biotin ligase (BirA) from *E.Coli* (PDB ID:1HXD) for designing split pBirA pairs in Figure 1. Based on B-factor information (**Appendix A**), we visualized it using PyMOL (http://www.pymol.org).

Ⅲ. Results

3.1 Design of MCS-ID

To develop the split system, we employed molecular dynamics analysis (**Figure 2** and **Appendix A**) based on the crystal structure of biotin ligase (BirA) to select the most flexible loop region as a cutting site to minimize deformation of the structural integrity of the natural enzyme. As shown in **Figure 3**, we selected 4 candidate cleavage sites (I64, G78, L262, and K283), based on the conformational flexibility and domain. Next, we tagged the N- and C- termini fragments of pBirA (e.g., N-pBirA and C-pBirA), which were divided by the selected cleavage sites to generate the FRB and FKBP proteins, respectively. Because hetero-dimerization of FKBP- and FRB-conjugated proteins can be easily induced by the addition of rapamycin to live cells[26,27], we could screen the split pairs of pBirA whose biotinylating activity was restored after protein complexation by conjugated protein–protein interactions, not by the intrinsic affinity between the split fragments (**Figure 4**). The intrinsic affinities of split fragments have been reported for several split reporter systems[6, 28] and enhanced activity is observed in some cases[29-30]. However, splitting the MAM system should result in reduced intrinsic affinity and significantly impaired cellular physiology because artificial MAM formations are known to increase the mitochondrial local calcium concentration[31-32], which can compromise mitochondrial oxidative capacity and augment oxidative stress. Thus, we desired to select for functional split pBirA fragments that possessed no intrinsic affinity at all.

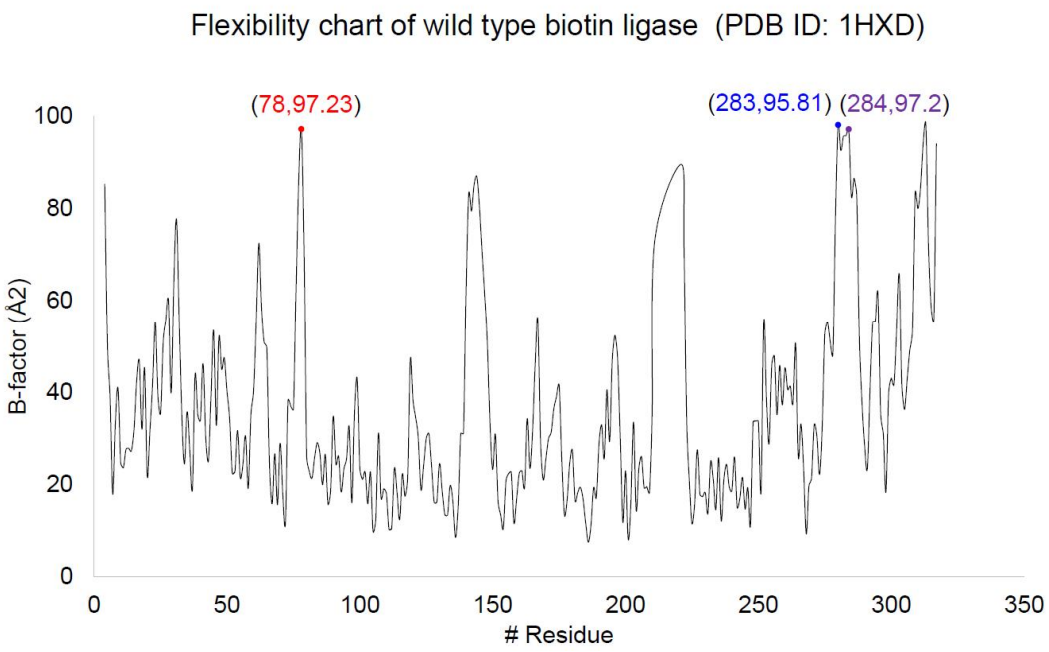


Figure 2. Flexibility chart of biotin ligase and screening test of 4 pairs of split pBirA. B-factors which represent flexibility corresponding to each amino acid. Highest B factors are 97.23 at G78 and 97.2 at E284. Based on flexibility, G78 and E283 were selected as split position of pBirA. All B-factors for Cα are also written in **Appendix A**.

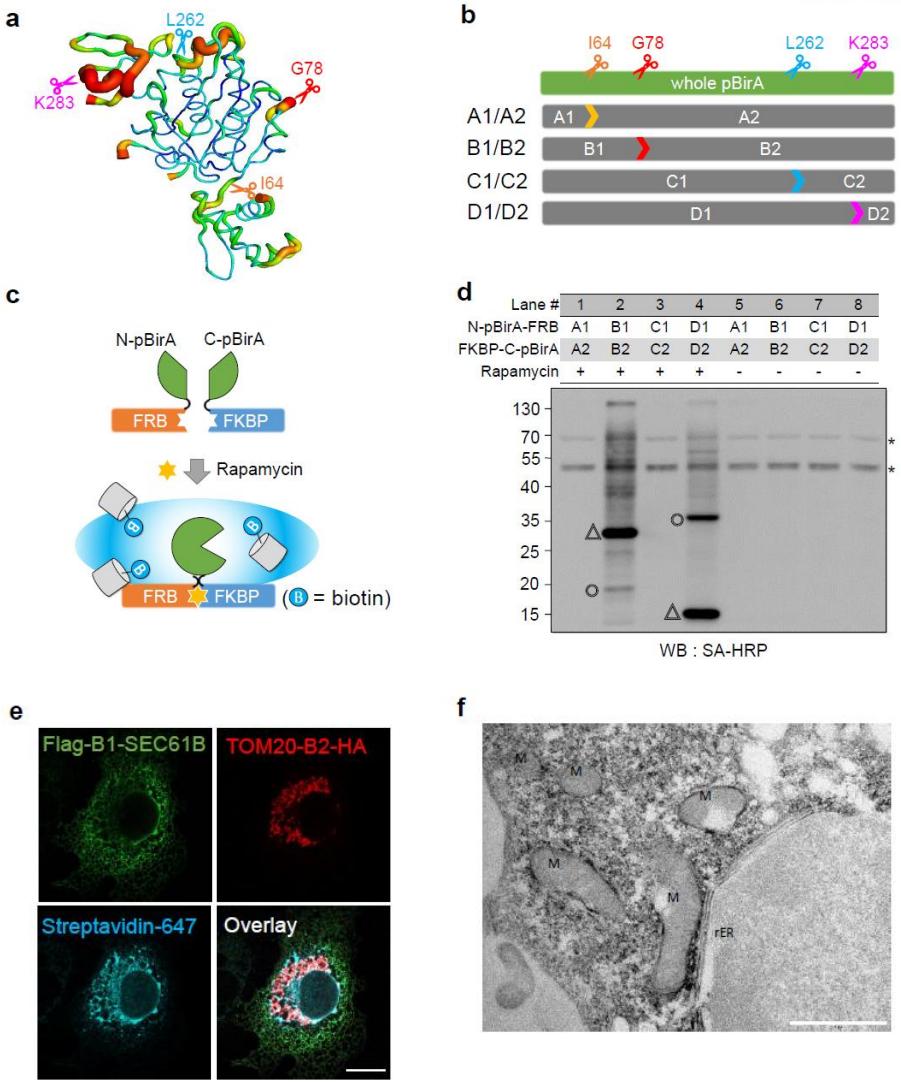


Figure 3. Design of MCS-ID and application for MAM.

a. Tube representation of conformational flexibility in pBirA and schematic overview of the split pBirA pairs. From A to D, 4 sites have been chosen depending on conformational flexibility (B, D) and domain (A, C). **b**. Schematic overview of screening the split pBirA pairs. Rapamycin dependent heterodimerization of FKBP and FRB was introduced into the screening. Among 4 pairs, only B and D, which are designed based on flexibility, were promising and B pairs with less intrinsic affinity than D pairs were finally selected. **c**. Schematic reconstitution of the split pBirA in FKBP-FRB system. **d**. Screening of split pBirAs and promising result from B and D pairs. Circle indicates N-pBirA-FRB and triangle indicates FKBP-C-pBirA. Asterisk indicates endogenous biotinylated proteins **e**. localization of biotinylated protein by MCS-ID in confocal microscopy resolution. Scale bar, 20um. **f.** localization of biotinylated protein by MCS-in EM resolution. Scale bar, 1um.

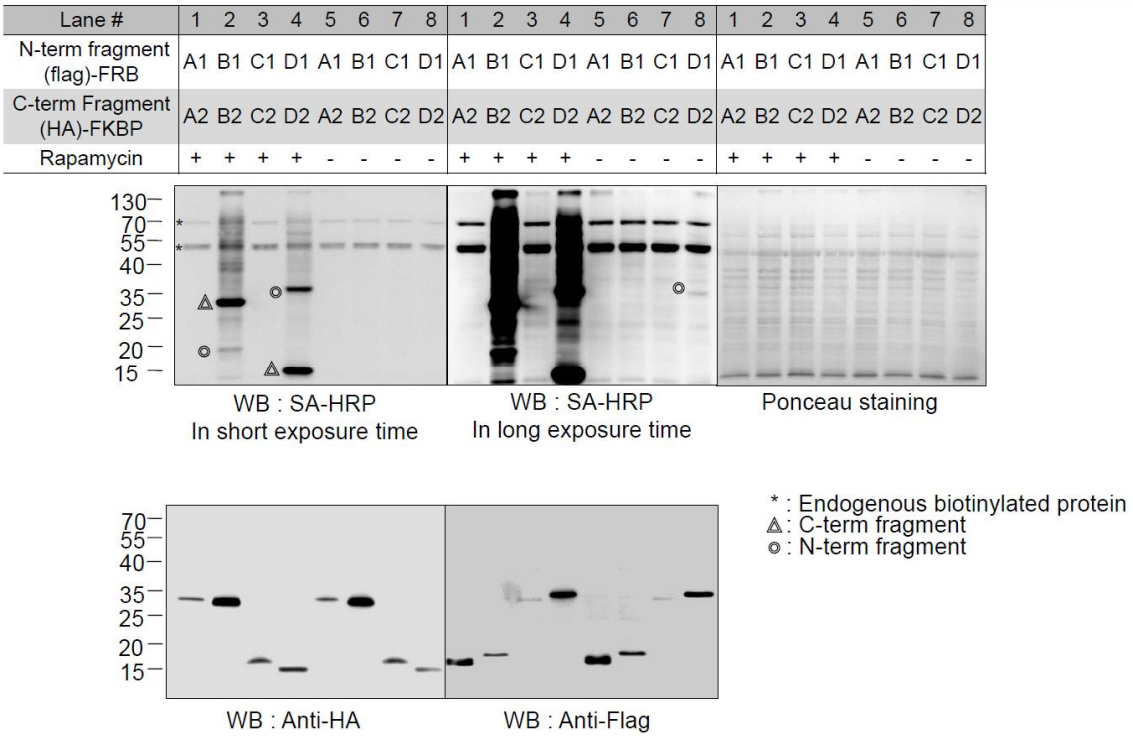


Figure 4. Comparison of biotinylation activity and expression level for split pBirA systems. Biotinylation activity of each split sites measured by western blot signal using Streptavidin-HRP. Loaded protein amount shown by ponceau staining. Expression level of each split pBirA fragments measured by western blot signal using flag and HA antibodies. Comparing with B pairs, D pairs showed little intrinsic affinity thus, all following experiment were done with B pairs and named as MCS-ID.

Among our attempted constructs, we observed that the split pBirA pair (N-G78 and G79-C) showed considerable biotinylating activity in the presence of rapamycin (100 nM), and these constructs showed no biotinylating activity under the control condition (e.g., no rapamycin treatment) (**Figure 3b** and **4**). These results indicated that this paired system may not spontaneously form an active structure, possibly owing to a very low intrinsic affinity toward each other. Data from immunoprecipitation experiments confirmed that the split pBirA pair (N-G78 and G79-C) did not physically interact with each other (**Figure 5**), while other constructs such as the split pBirA pair K283-E284 showed detectable intrinsic binding affinity (**Figure 1** and **4**). Thus, our proposed pair system (N-G78 and G79-C) represented a significantly improved system compared with previously reported systems, indicating that it may be employed in organelle-contact site mapping. Thereafter, we used the (N-G78 and G79-C) paired system for subsequent experiments and named the paired system MCS-ID.

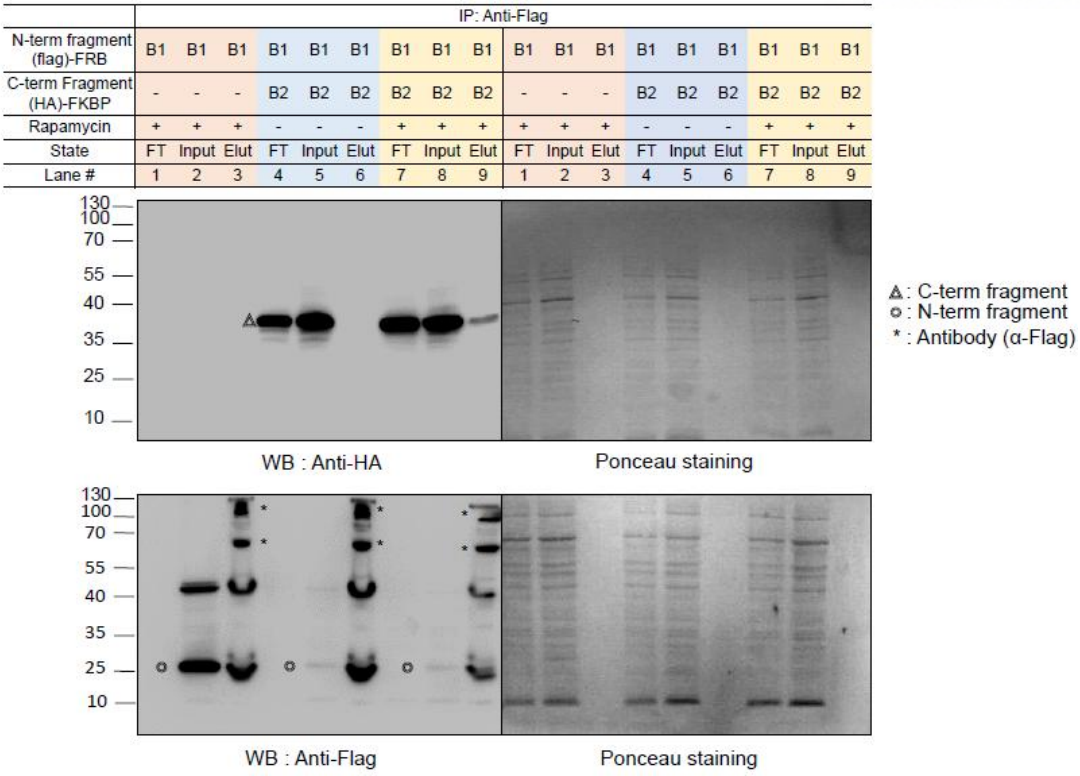


Figure 5. Validation of intrinsic affinity in MCS-ID.

Following immunoprecipitation experiment as **Scheme 2,** Intrinsic affinity of MCS-ID was validated thoroughly. Negative controls were done without C-terminus fragment of split pBirA. Positive controls were done by treating rapamycin for inducing FKBP-FRB heterodimerization.

3.2 Identification of the MAM proteome by MCS-ID

We designed ER cytosolic face membrane (ERM) and outer mitochondrial membrane (OMM) constructs by genetic fusion of N-pBirA and C-pBirA to SEC61B and TOM20, respectively. Because TOM20 and SEC61B are abundant proteins at each membrane and these proteins have no intrinsic binding affinity for each other, we expected to observe selective biotinylation of these recombinant proteins in an enforced-interaction environment at the ERM and OMM contact sites. To test this possibility, we imaged COS-7 cells co-expressing ERM-N-pBirA and OMM-C-pBirA. As shown in **Figure 3e**, we observed that a biotinylated pattern (detected using Alexa Fluor 568-conjugated streptavidin) occurred between ERM-N-pBirA and OMM-C-pBirA. Furthermore, we visualized these biotinylated proteins by electron microscopy (EM) imaging after diaminobenzidine (DAB) staining using streptavidin-HRP (detailed procedures are in the **Experimental methods & Materials**). We found that most biotinylated proteins localized between OMM and ERM, indicating that MCS-ID functioned at the ER-mitochondrial contact site (**Figure 3f**). Next, we were interested in analyzing the proteins biotinylated by ERM-N-BirA and OMM-C-pBirA via mass spectrometry (MS). For this experiment, we employed our previously developed mass analysis method (Spot-BioID), which focuses on MS/MS spectra by searching for peptides containing biotinylated lysine (K+224 Da), directly labeled by pBirA (**Figure 6a**)[33]. Thus, we could selectively identify biotinylated proteins from complemented pBirA at the ER-mitochondrial junction using our BioClap method. We conducted replicate experiments with these constructs of TOM20 (OMM) + SEC61B (ERM), and only reproducibly biotinylated proteins were finally included in our list. For control experiments, we also collected biotinylated peptide information from ERM-pBirA, OMM-pBirA, and untargeted EGFP-pBirA samples under non-starvation and starvation conditions (**Figure 6b, c** and **Appendix B**). From the proteins identified using the MCS-ID system, we filtered out doubly detected biotinylated proteins with untargeted pBirA (e.g. EGFP-pBirA) because these biotinylated proteins could be preferentially labeled by pBirA, regardless of its sub-cellular localization. We also filtered out biotinylated proteins (PC, PCCA and MCCC1) by endogenous biotin ligase. Following this stringent analysis, we identified 72 MAM proteins that were exclusively observed in the MCS-ID samples over EGFP-pBirA (**Figure 6d**).

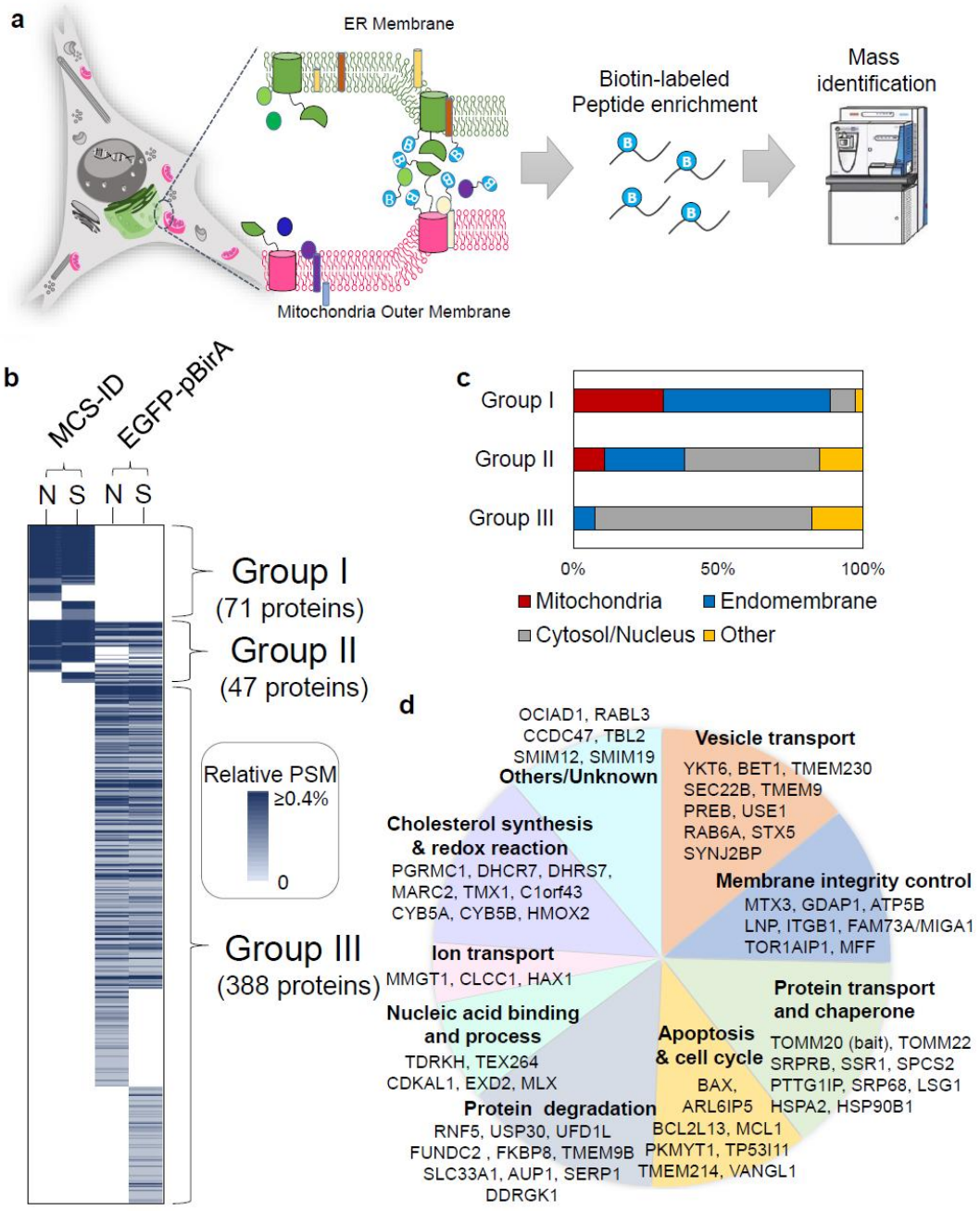


Figure 6. Schematic view of MAM proteome profiling and characteristics of MAM proteome revealed by MCS-ID.

a. Schematic view of MCS-ID used for MAM proteome labeling and profiling. **b.** Heatmap of labeled proteins by MCS-ID and EGFP-pBirA. N represents normal condition and S represent starvation condition. Group I (exclusively detected in MCS-ID), Group II (overlapped in MCS-ID and EGFP-pBirA), Group III (exclusively detected in EGFP-pBirA). **c.** Composition of each group corresponding to its subcellular localization. **d.** Proteins in Group I were classified by its functions.

Using the strength of the MCS-ID system in identifying MAM proteins, we further tested whether MCS-ID was applicable under specific physiological conditions, such as nutrient starvation. Because MAM is known as the location for the early stages of autophagy under starvation conditions[5], we were interested in checking which proteins could be temporally detected at the MAM under starvation conditions using our technique. For this purpose, we conducted MS analysis of MCS-ID samples along with control samples of ERM-pBirA, OMM-pBirA, and EGFP-pBirA, under fetal bovine serum (FBS)-starvation conditions[34] for 12 h. Following stringent analysis mentioned above, we identified 62 proteins that did not overlap with the cytosolic EGFP-pBirA sample in the starved condition. These data were comparable with the non-starvation MCS-IDome, and we could classify MAM-resident (47 proteins) and temporal MAM-resident proteins found only during starvation conditions (14 proteins) or only during non-starved conditions (11 proteins).

It is also noteworthy that most of the MCS-IDome was found either by the ERM- or OMM-whole pBirA, and this result is reasonable considering that MAM-resident proteins should have originated from the ERM and OMM. However, we found that relative Peptide Spectrum Match (PSM) values (e.g., the identified PSM value of each protein divided by the total PSM value) in the MCS-IDome did not follow the relative PSM values, either in the dataset of ERM-pBirA or OMM-pBirA. The scatter plots of the relative PSM values between the MCS-IDome and the ERM- or OMM-pBirA dataset showed low correlation R^2 values (with ERM: 0.0002; with OMM: 0.1272; **Figure 7**). These results indicated that the MAM proteome was composed of selective ERM and OMM proteins, rather than a combination of abundant ERM and OMM proteins.

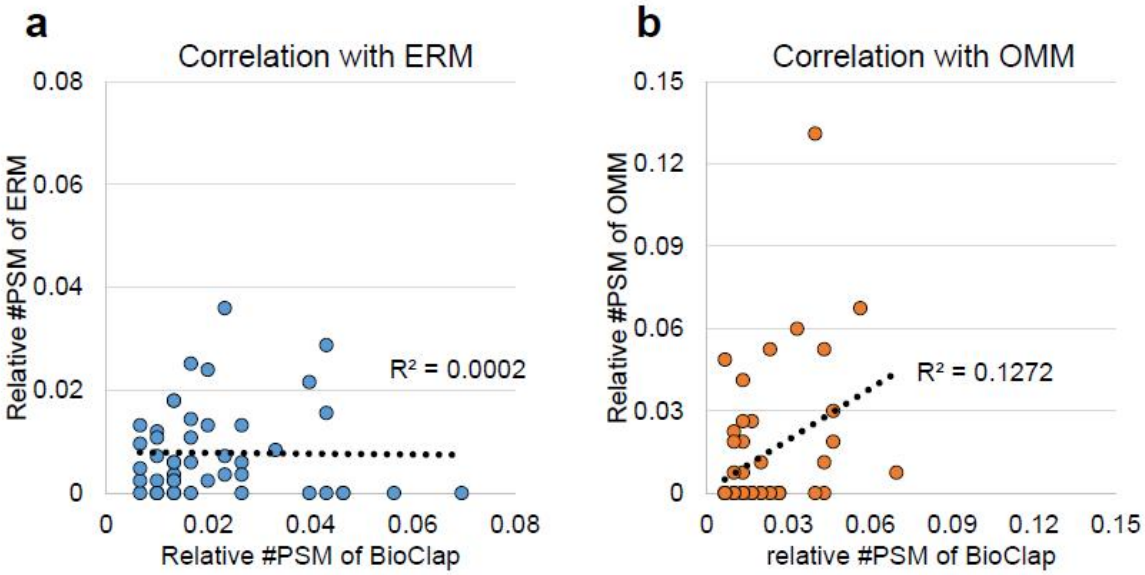


Figure 7. Correlation of relative #PSM in MCS-IDome with ERM proteome, OMM proteome. Negligible correlation between MCS-IDome and ERM, OMM proteome. Relative PSM number of 72 proteins found in MAM was compared with those in ERM-pBirA and OMM-pBirA. Scatter plot showed there is little correlation with each other and R^2 values are also relatively negligible as 0.0002 (ERM) and 0.1272 (OMM), respectively.

3.3 CYB5B and FKBP8 dually localized at the ER and mitochondria via MAM

We observed 2 groups of MAM-resident proteins related to starvation. One group was comprised of permanent MAM residents and the other group was comprised of temporal MAM residents, and these proteins were only detected under starvation or non-starvation conditions, respectively. Based on DAVID gene-function analysis[35] of the MCS-IDome, several heme-binding proteins (e.g., CYB5A, CYB5B, HMOX2, and PGRMC1) and ER-to-Golgi vesicle mediated transport-machinery proteins (e.g., YKT6, BET1, STX5, and SEC22) were enriched in the MAM protein list. This result implied that active heme metabolism and SNARE protein complex formation might be mediated at the MAM. It is noteworthy that HMOX2 and STX5 were identified as temporal MAM-resident proteins that were only labeled by the MCS-ID system under the starvation condition.

To confirm that these proteins indeed localized to the MAM, we transfected a construct encoding CYB5B-EBFP (EBFP attached to the N-terminus of CYB5B) in COS-7 cells. In this experiment, we also introduced GFP-SEC61B and TOM20-mApple as ERM and OMM marker proteins, respectively. In addition, we conducted control experiments with Mito-EBFP and EBFP-KDEL, which employed signal sequences known to target conjugated tag proteins to the mitochondrial matrix and ER lumen, respectively.[36] As shown in **Figure 8**, EBFP-CYB5B showed an intermediate localization pattern between the ER and mitochondria, with significant overlap both with OMM-marker and ERM-marker proteins and Pearson's correlation values (P) of 0.66 and 0.38, respectively. In control experiments, Mito-EBFP showed exclusive overlap with the OMM marker (P = 0.81), and EBFP-KDEL showed exclusive overlap with the ERM marker (P = 0.97), while these controls showed negligible overlap with other organelle markers (**Figure 8b, c**). These results indicated that CYB5B localized mainly at the mitochondria, but was also localized at the ER. We postulated that CYB5B might be labeled by MCS-ID during its translocation from the OMM to ER via MAM. It is noteworthy that CYB5B is known to form an amidoxime reductase complex with MARC2[37], and MARC2 was also found in our MCS-ID list as a permanent resident, implying that amidoxime reduction metabolism might be stably mediated at the MAM.

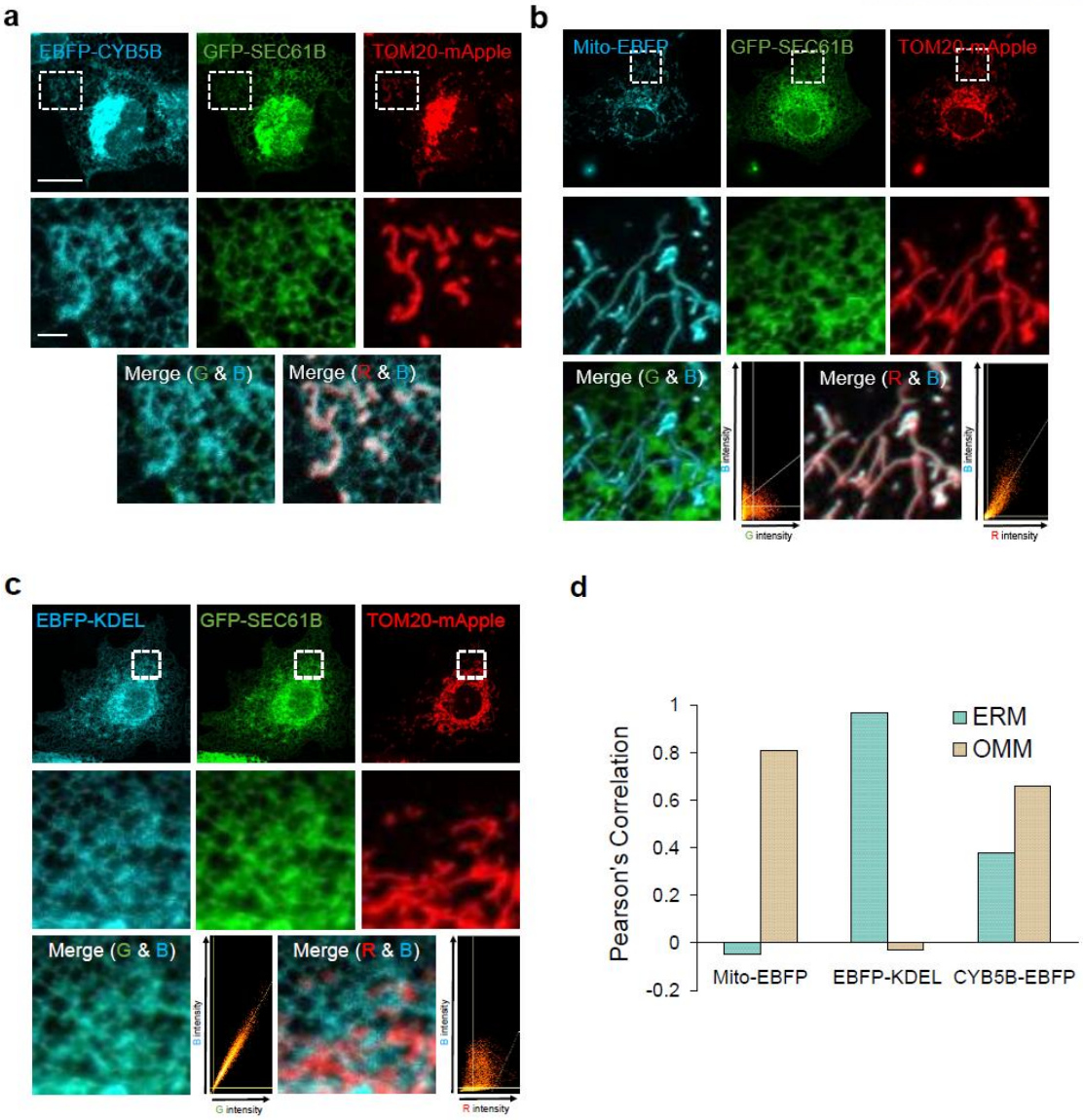


Figure 8. Correlation of CYB5B with ERM and OMM compared with controls.

a. Localization of CYB5B with ERM (GFP-SEC61B) marker and OMM (TOM20-mApple) marker. **b.** Mitochondiral matrix marker as Mito-EBFP was correlated with ERM and OMM markers, repectively. **c.** ER matrix marker as EBFP-KDEL was correlated with ERM and OMM markers, repectively. For **a-c.**, Scale bars for low magnified images, 20um. Scale bars for high magnified images, 2um. **d.** As shown in confocal image in **a.**, comparing ER and mitochondrial matrix marker, CYB5B showed modest correlation with ERM and OMM markers.

We also examined the subcellular location of FKBP8, which was in the MCS-ID list as a permanent MAM-resident protein and was labeled by ERM and OMM-pBirA. Because FKBP8 is an OMM protein that can be dynamically transported from the OMM to the ERM during mitophagy [38], we postulated that FKBP8 should localize near the ER–mitochondrial junction for efficient translocation from the OMM to the ERM. To test this hypothesis, we attempted to image the subcellular localization of FKBP8 via EM by generating a fusion between FKBP8 and engineered ascorbate peroxidase 2 (APEX2), which could be imaged by EM after DAB polymerization and osmium tetroxide (OsO_4) staining[39]. For this experiment, we prepared APEX2-FKBP8 and FKBP8-APEX2, with APEX2 conjugated to the N-terminus or C-terminus of FKBP8, respectively. Because FKBP8 has a transmembrane helix region at the C-terminal domain, it was expected that OMM targeting of FKBP8-APEX2 should be compromised. EM images (**Figure 9a**) revealed that the DAB/OsO_4 staining region of APEX2-FKBP8 was localized at the OMM, which was surrounded by ER tubules. This result indicated that APEX2-FKBP8 mainly localized at the MAM. Interestingly, we observed that DAB/OsO_4 staining of FKBP8-APEX2 occurred at the ER lumen and its tubules were surrounded by mitochondria (**Figure 9b**). This result indicated that the membrane topology of FKBP8 was the same at the OMM and ERM, with the N-terminal domain localized to the cytosolic space. We postulated that a TM region of FKBP8-APEX2 might be subsequently recognized by unknown ER membrane translocation machinery, such as a tail-anchoring protein complex[40] near the OMM, which process might be an intriguing topic of research in a future study (**Figure 9c**). Furthermore, we also postulated that the cytosolic domain of FKBP8 might be related to generating more ER–mitochondria-tethered junctions because FKBP8-transfected cells showed more mitochondria and ER clusters, compared with control cells (overexpressed proteins targeting to ER lumen) in **Figure 9d**.

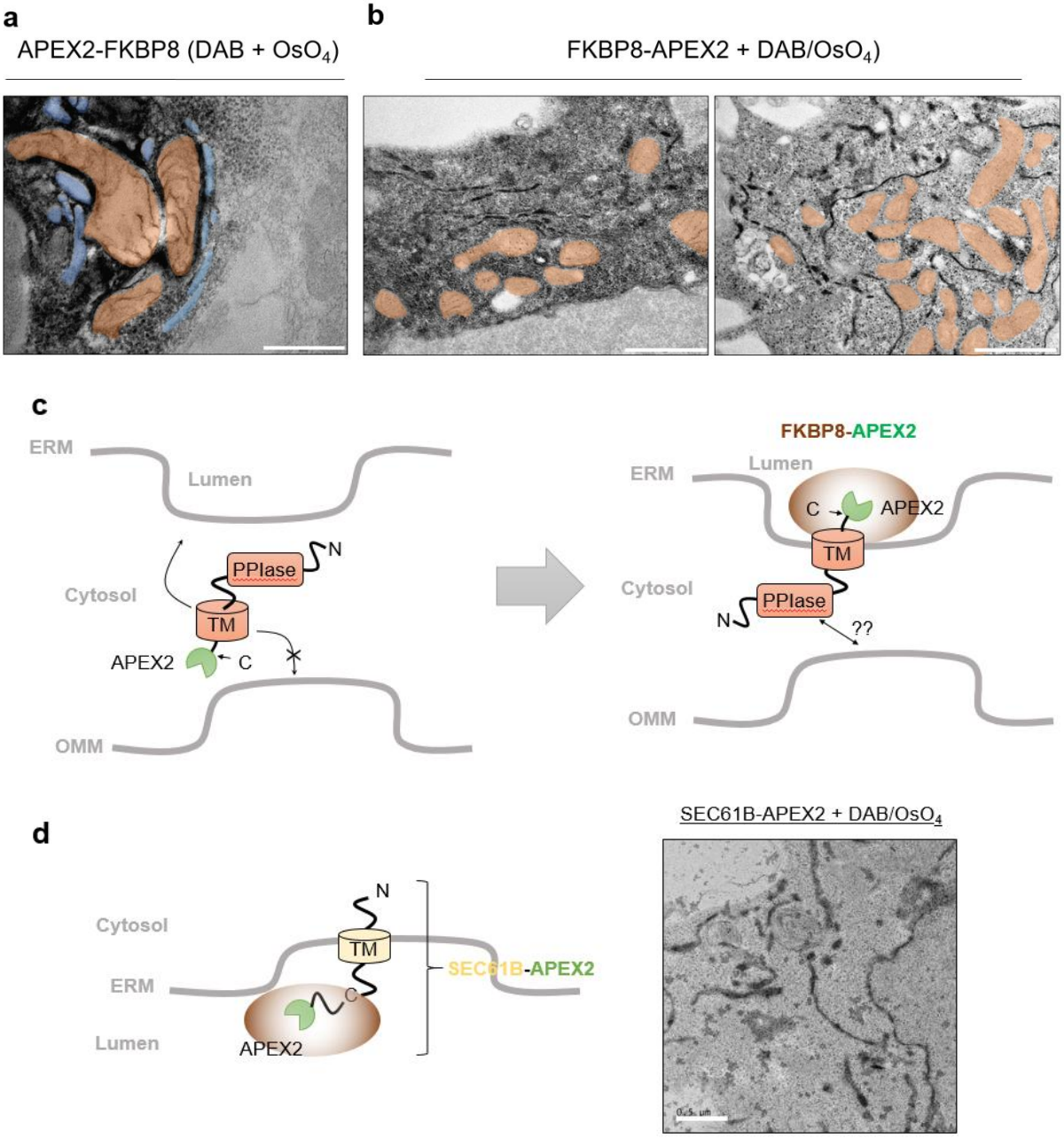


Figure 9. Localization of FKBP8 tagged by APEX2 in EM imaging and control image. **a.** Localization of FKBP8 as interface with ERM and OMM in EM imaging. N-terminus of FKBP8 tagged with APEX2 lead to localize at OMM near by ERM. Mitochondria is colored by orange and ER tubule is colored by blue. Scale bar, 500nm. **b.** ER localized FKBP8 tagged by APEX with C-terminus of it. Many mitochondria were also shown nearby FKBP8. Scale bar 1um. **c.** Hypothetical mechanism of mislocalization of FKBP8-APEX2. **d.** As control, SEC61B tagged with APEX2, were shown ER tubules in EM imaging and nearby mitochondria were unobservable. Scale bar, 500nm.

3.4 The peroxisomal membrane protein ABCD3 localized to the MAM

In our MCS-IDome, we also identified ABCD3 (also known as PMP70), which was also labeled both by ERM- and OMM-whole pBirAs. ABCD3 is a peroxisome membrane protein related to peroxisome biogenesisis[41-42]. Peroxisome is known to originate from the ER membrane[43], and it was recently shown that mitochondria-derived vesicles merged with peroxisomes[44]; however, its relationship with the MAM has rarely been reported. To determine whether ABCD3 localized at the MAM, we imaged ABCD3 with a primary antibody, and we also imaged mCherry-KDEL, Mito-EBFP, and PEX3-EGFP as marker proteins for the ER, mitochondria, and peroxisome, respectively. **Figure 10** shows that ABCD3 and PEX3-EGFP highly overlapped with each other; however, we found that ABCD3 more closely localized to the intermediate space between the ER and mitochondria, as shown in the 3D-reconstructed confocal images (**Figure 10b**). This minor discrepancy between ABCD3 and PEX3 might have been caused by multiple organelles targeting ABCD3[45], and we postulate that ABCD3 might play a role in pre-peroxisomal vesicle formation at the MAM. Further studies are required to test this hypothesis. Similar in yeast, interaction between PEX11 of peroxisomal proteins and Mdm34 of ERMES complex (which localized in ER-Mito contact sites) has been found recently[46-47] and thought to be essential for efficient fatty acid β-oxidation process. Although, to the best of our knowledge, there is no report about interaction between peroxisome and MAM in mammalian cells yet, this founding will facilitate the discovery of new aspects in cell biology.

It is noteworthy that several other endogenous peroxisomal proteins such as PEX5, PEX14, and PEX19 were labeled by Tom20-pBirA for 24 h in **Appendix C**. These proteins were not observed after a 12-h labeling by Tom20-pBirA, which might indicate they were temporarily localized at the OMM. Among these proteins, PEX5 and PEX19 were also found after a 24-h labeling by ERM-pBirA (**Appendix C**). Interestingly, PEX14 was demonstrated to localize first at the OMM, based on extensive imaging experiments by McBride and colleagues[48]. Thus, our finding of peroxisomal proteins at the OMM support the possibility that the OMM is a key subcellular space for peroxisome biogenesis.

In order to confirm that our method is on the extension in the way of obtaining the MAM, subcellular fractions by Percoll centrifugation were obtained as conventional method. GRP75 as one of widely used MAM marker and PMP70, CYB5B were found at MAM fractions by immunoblot. Compared with GRP75, furthermore, PMP70 and CYB5B showed more intense localization on MAM (**Figure 11a**). For verify subcellular fractions, 4 subcellular markers (VDAC1, COXIV, PDI, β Tubulin) were also used (**Figure 11b**).

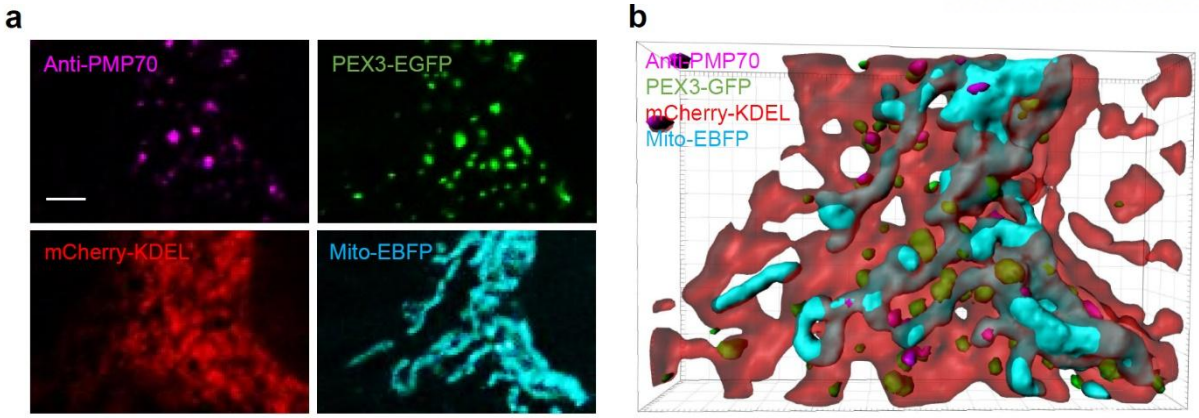


Figure 10. Localization of PMP70 via confocal microscopy and validation by conventional fractionation.

a. Localization of PMP70 colored in magenta and ER (KDEL), Mitochondria(Mito), peroxisome(PEX3) markers in confocal imaging. Scale bar, 2um. **b.** Compared to PEX3, more closer localization of PMP70 shown between ER and mitochondria in 3D reconstruction.

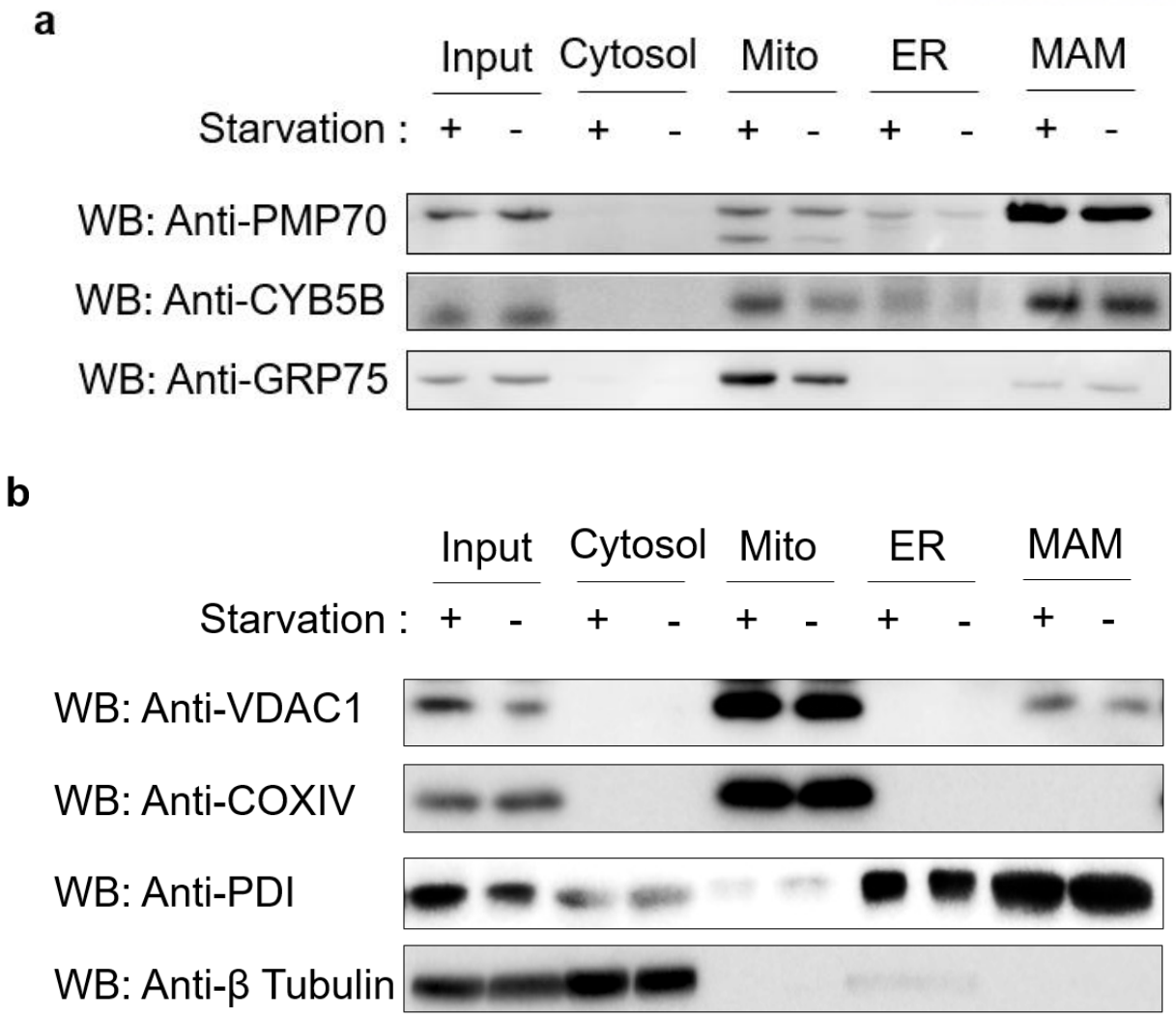
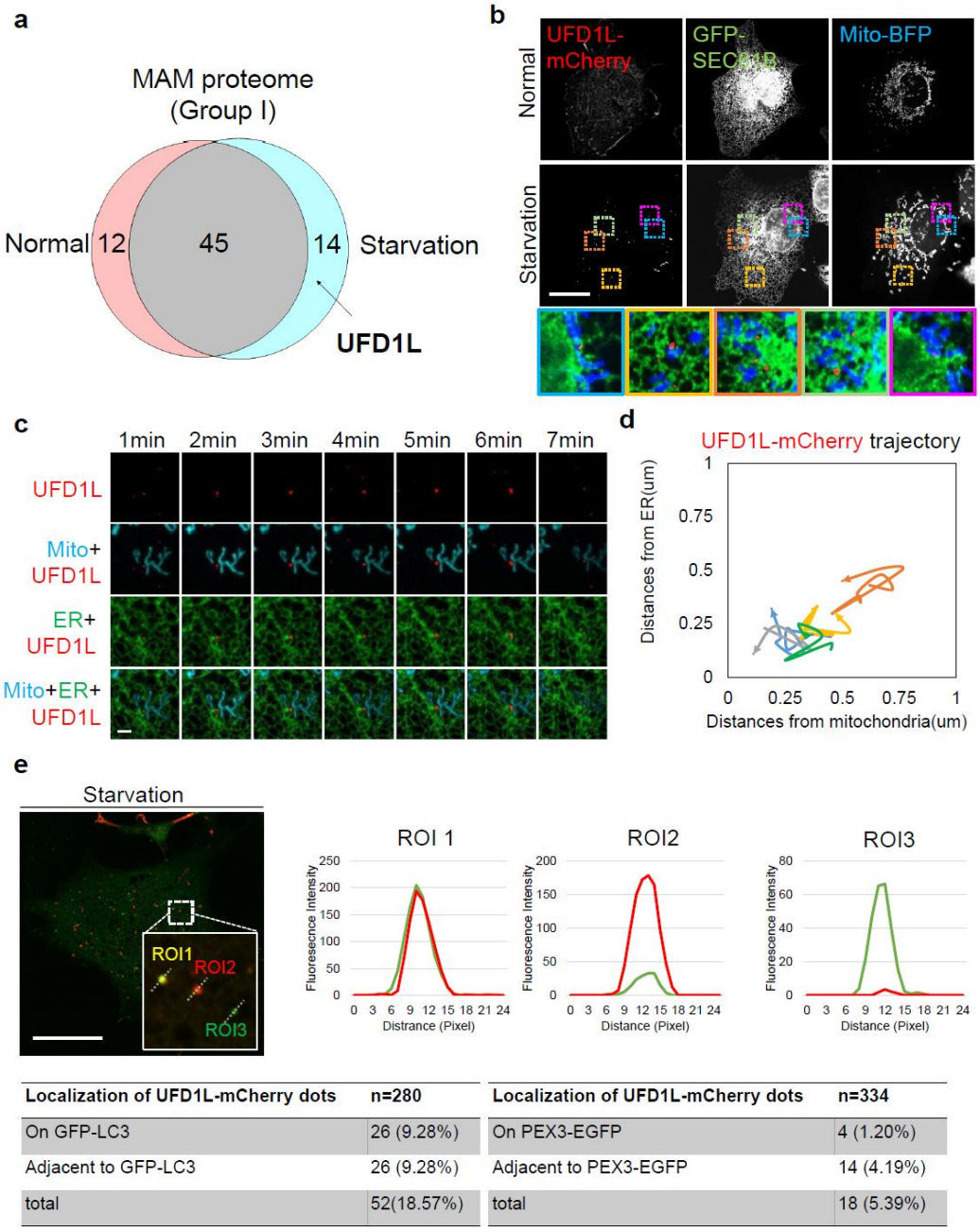


Figure 11. Validation of CYB5B and PMP70 by conventional fractionation method.
a. After Fractionation, PMP70, CYB5B detected through western blot. GRP75 was used as conventionally validated MAM target in fractionation. Compared with GRP75, PMP70 and CYB5B showed more significant MAM localization. **b.** Fractionation specificity verified with 4 proteins (VDAC1: OMM protein, COXIV: mitochondria inner membrane protein, PDI: ER protein, β Tubulin: cytosolic protein.)

3.5 Starvation induced UFD1L localization at the MAM

It is well-known that many cellular processes are reorganized during starvation for survival purposes, with one prominent process being autophagy[49-50]. Recently, it was reported that several key proteins involved in autophagosome formation are recruited to the MAM during the initial stage of autophagy[5]. However, proteome changes at the MAM have not been systemically analyzed because of a lack of an effective method to isolate the MAM proteome without false positives. Thus, we attempted to monitor starvation-induced proteome changes at the MAM using the MCS-ID system. Comparing MCS-ID identified proteins associated with starved and non-starved conditions revealed that some proteins were observed specifically under starvation conditions (24 proteins), but not under non-starvation conditions in replicate experiments and vice versa (**Figure 12a**). Among these proteins, we found that several ubiquitin-related proteins such as UFD1L (ubiquitin fusion degradation protein 1 homolog), RNF5 (E3 ubiquitin-protein ligase), and USP30 (deubiquitinating enzyme) were reproducibly labeled by the MCS-ID system at the MAM during starvation only. This result implied that ubiquitin-mediated process should be actively mediated at the MAM under the condition of starvation.

Among these proteins, we attempted to confirm whether UFD1L, an essential component of the ubiquitin-dependent proteolytic machinery, was temporally recruited to the MAM during starvation. For this experiment, we expressed UFD1L-mCherry along with GFP-SEC61B and Mito-EBFP as marker proteins for the ER and mitochondria, respectively. **Figure 12b** shows that UFD1L-mCherry formed a cytosolic or plasma membrane-localized pattern in the non-starvation condition, but punctate expression was observed after 12 h of FBS starvation. Further analysis of ER and mitochondrial marker protein localization revealed that most UFD1L-mCherry dots localized at the ER-mitochondrial interface (103 of 168, 61%), while other UFD1L-mCherry dots localized near the ER membrane (65 of 168, 39%).



Localization of UFD1L-mCherry dots	n=280
On GFP-LC3	26 (9.28%)
Adjacent to GFP-LC3	26 (9.28%)
total	52(18.57%)

Localization of UFD1L-mCherry dots	n=334
On PEX3-EGFP	4 (1.20%)
Adjacent to PEX3-EGFP	14 (4.19%)
total	18 (5.39%)

Figure 12. localization and dynamics of UFD1L and interaction with lysosome.

a. Ratio between starvation and normal condition in MAM proteome (Group 1). **b.** localization of UFD1L-mCherry in starvation and normal condition with ER and mitochondria marker. Scale bar, 20um **c.** Time course images of emergence of UFD1L-mCherry-dots with ER and mitochondria marker. Scale bar, 2um. **d.** Dynamics of UFD1L-mCherry dots in **c.** and **Supplementary Figure 1. e.** Co-localization of UFD1L-mCherry dots with GFP-LC3 (a lysosome marker). Scale bar, 20um. Quantification of co-localized UFD1L-mCherry dots with GFP-LC3 and PEX3-EGFP (a peroxisome marker). Dots located within 0.5um and 0.2um from each organelle are considered as 'adjacent' and 'on', respectively.

We also conducted live-cell imaging analysis with UFD1L-mCherry and found that the UFD1L-mCherry dots dynamically oscillated at the interface of the ER and mitochondria, with distance of <1 μm from both organelles during the 10 min after its formation at the MAM (**Figure 12c, d** and **Supplementary Figure 1).** We also conducted the following imaging experiment with the lysosome marker protein, GFP-LC3, to determine whether mCherry-UFD1L dots overlapped with lysosomal vesicles. As shown in **Figure 12e** and **Supplementary Figure 2**, we observed that 18% of UFD1L-mCherry dots localized adjacent to or with GFP-LC3, while a negligible portion (5.4%) of UFD1L-mCherry dots localized nearby the peroxisome marker protein, PEX3-GFP. Data from imaging experiments with GFP-LC3, EBFP-KDEL (ER), and anti-TOM20 (mitochondria) showed that UFD1L-mCherry dots formed 2 separated populations at the MAM and the lysosome. Although it is not fully characterized whether UFD1L-mCherry dots are membrane-enclosed vesicles, we postulated previously that UFD1L complexes might be initially formed at the MAM and finally merge with lysosomes, as occurs in the autophagosome life cycle[51-52]. It might be intriguing to show a possible correlation between autophagosome formation and ubiquitin-mediated processes during starvation. Furthermore, UFD1L is known as an adaptor protein for the VCP complex, which mediates ER-membrane protein degradation and OMM protein degradation[53-55].Although VCP complex is known to degrade ER-membrane and OMM proteins, there is no approach to explain it via MAM localization. Thus, we hypothesized that if UFD1L as one of VCP complex localized at MAM, efficient degradation of OMM and ER-membrane proteins is possible compared with separately localized at ER-membrane or OMM. We think this hypothesis correlated with our finding which ubiquitin related enzymes including UFD1L, RNF5, USP3 gather into MAM to ubiquitinylate its substrates. Following degradation pathway can be suggested like proteasome or autophagy assisted pathway or through mitochondria-derived vesicles[56].(summarized in **Figure 13**). Further investigation of UFD1L related to mitophagy might be required to prove this hypothesis in the future.

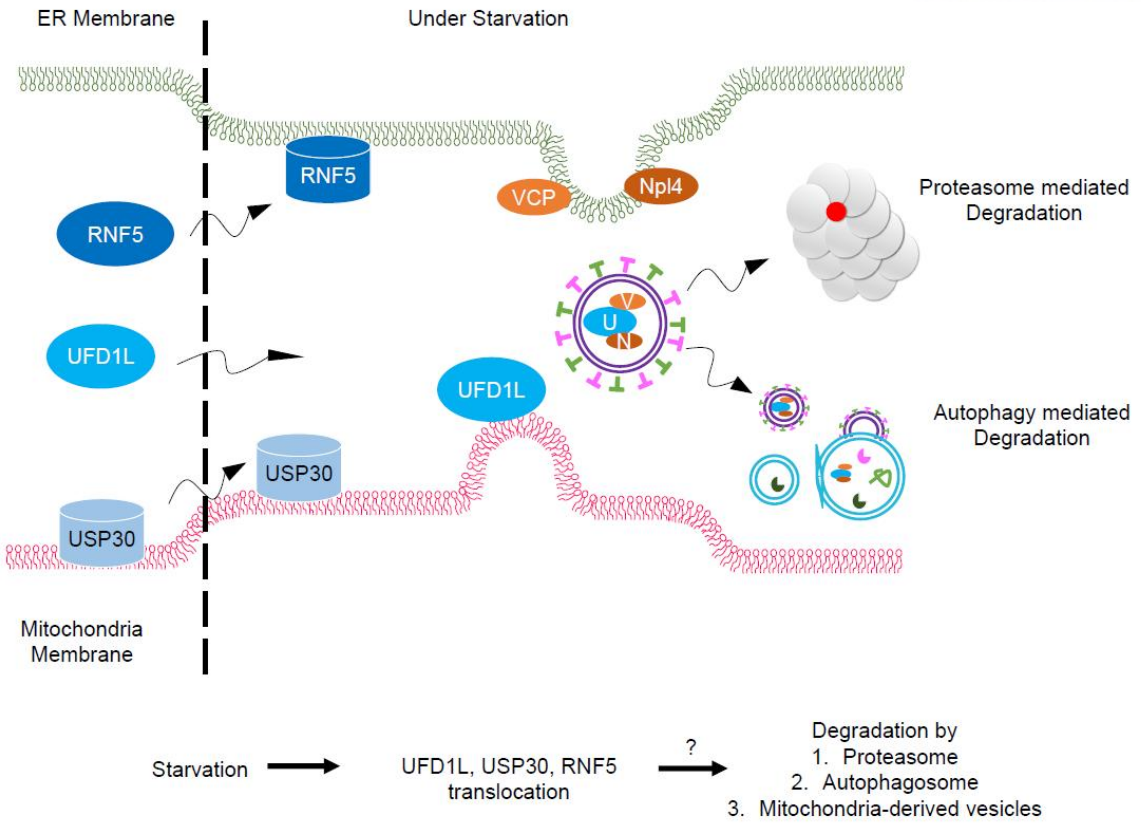


Figure 13. Proposed model for starvation induced translocation of ubiquitin related proteins. Schematic illustration of ubiquitin related proteins; UFD1L, USP30, RNF5. By specifically labeling under starvation condition, UFD1L is thought to be translocated in the MAM for efficient complex formation with VCP and Npl4 present in the ER. Similar to UFD1L-VCP-Npl4 complex, USP30 and RNF5 are thought to be involved into the protein degradation pathway. Although it is unclear how ubiquitin related proteins go into detail degradation pathway, translocation of under starvation condition suggest changes of protein degradation mechanism.

3.6 ATP5B accumulated at the OMM during starvation

In our experiments, we utilized OMM and ERM-whole pBirA data as a confirmation of our MCS-ID labeled protein localization, either at OMM or at ERM. By analyzing the protein-labeling data from the OMM and ERM-pBirA obtained during either the non-starvation condition or the starvation condition, we realized that these data could also be useful for understanding proteomic changes occurring at either the ERM or OMM under the starvation condition. For example, we observed that ATP5B showed greater labeling by TOM20-pBirA (OMM-pBirA) under the starvation condition (total PSM #21) than in non-starved condition (total PSM #13). Because ATP5B is a well-known mitochondrial matrix protein and a component of the ATP Synthase F_1 complex, we postulated that this protein should be biotin-labeled during mitochondrial translocation from the OMM to the matrix via the TOM translocation channel. However, it is unclear why this protein was more labeled at the OMM under the starvation condition. Because its total expression level was not changed by starvation, we hypothesized that its mitochondrial matrix translocation occurred efficiently during starvation, and ATP5B accumulated at the OMM might have a greater chance to be labeled by TOM20-pBirA.

To test this hypothesis, we cloned the ATP5B–APEX2 and examined its sub-mitochondrial location by its biotin-phenoxyl radical pattern generated in live cells[40]. We found that the ATP5B–APEX2 complex showed a very restricted biotin-phenoxyl radical labeling pattern under normal conditions, which indicated that the ATP5B–APEX2 complex was well translocated to the mitochondrial matrix under the non-starved condition. However, we observe that a portion of the ATP5B–APEX2 complex showed a very diffuse biotin-phenoxyl radical labeling pattern under the starvation condition, even with localization pattern at the mitochondria (**Figure 14**). This result implied that transport of the ATP5B–APEX2 from the cytosol to OMM occurred; however, its translocation from the OMM to the mitochondrial matrix failed under the starvation condition. Thus, the loss of membrane potential at the OMM under the starvation condition might cause this result, as reported previously[57-58]. Our data suggest that other mitochondrial proteins (e.g. FKBP8, MAVS, TOMM22, OCIAD1[59] and TDRKH[60]), which were labeled more by TOM20-pBirA under the starvation condition than the non-starved condition, might be related to translocation failure by starvation. We postulate that these untargeted proteins at the OMM might be targeted for protein degradation or mitochondrial quality control at the MAM, although further investigation is required to characterize these processes.

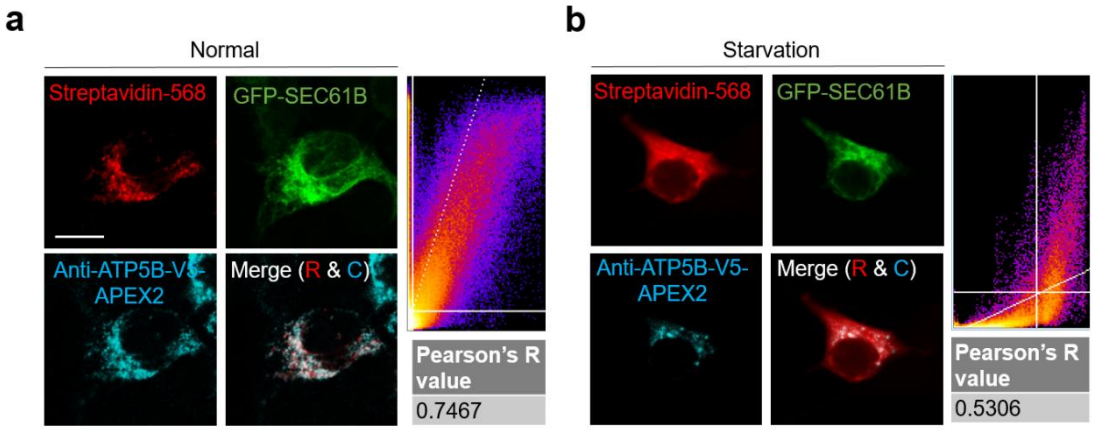


Figure 14. translocation of ATP5B-APEX2 under normal and starvation condition. Biotinylation pattern (Red) and localization (Cyan) of ATP5B-APEX2 and ER marker (Green, GFP-SEC61B) under normal (**a**) and starvation (**b**) condition. Scale bar, 20um. Translocation of mitochondrial matrix protein, ATP5B, into outer mitochondrial membrane under starvation condition. Biotin phenol activated by APEX2 could be diffusive out into cytosol when ATP5B tagged by APEX2 was translocated OMM. Streptavidin-568 capturing biotinylated protein showed higher (R value, 0.7467) correlated localization to mitochondria but starvation induced lower correlation (R value, 0.5306).

Ⅳ. Discussion

In this study, we found that the MAM was closely related to the biogenesis of 2 intracellular vesicles mediating peroxisomal protein translocation and ubiquitination processes. Follow-up imaging experiments showed these 2 MAM-derived vesicles did not highly overlap with each other (**Figure 12e** and **Supplementary Figure 2**). Because MAM is known to have a "lipid raft" property[21, 61], we postulate that the membrane protein components of those MAM-derived vesicles can be initially clustered at the MAM. However, it is largely unknown how this process is spatiotemporally regulated within cells. Further investigation is required to clarify this process.

Currently, the pBirA-labeling method or BioID has been widely utilized in various clustered proteomics identification studies. Because the original method, BioID, may generate false-positive findings from non-biotinylated proteins that possess strong binding affinity toward biotinylated proteins, we utilized an advanced identification method, Spot-BioID, to directly study the biotin-labeled peptidome from various sub-cellular localized pBirA proteins, without generating false positives. From this analysis, we found an unexpected feature of labeling pBirA, in that several proteins were consistently labeled by pBirA regardless of their localization. For example, PGRMC2, SNAP29, PFN1, PC, TAGLN2, TMPO, CRK, EIF5, VAMP2, CLINT1, MAVS, ARFGAP1, CDCA3, NUCKS1, PNN, and WWOX were identified in all our pBirA experiments (e.g., MCS-ID, OMM-, ERM-, cytosolic-pBirAs) under both non-starvation and starvation conditions. We postulate that the biotinylated domain of these proteins may have a specificity toward pBirA or biotin-AMP. We also found that several of these proteins were already identified in previous studies involving BioID[1, 62-63]. For example, the EIF5, TAGLN2, CRK, and WWOX proteins were labeled in several other studies using different subcellular targeted pBirAs[63-65]. Thus, we suggest that proteins in the pBirAome labeled using pBirA should be carefully confirmed by follow-up studies (e.g. imaging). In this study, we excluded all proteins labeled by cytosolic EGFP-pBirA from our MCS-IDome, ERM, and OMM lists.

We also found that sites that were biotin-labeled using the MCS-ID system are useful for identifying membrane protein topologies in live cells. Because pBirA labeling occurred at the cytosolic face of the ERM or OMM, the labeled site should be localized to the cytosolic side. Based on the identified membrane topologies in UniProt, we confirmed that the membrane topologies of 27 proteins matched well with our findings (**Figure 15** and **Appendix D**). Using our labeled-site information, we can propose membrane topologies for 25 proteins

including ABCD3, FKBP8, GDAP1, BAX, BCL2L13, and FAM73A, whose membrane topologies have not been fully characterized. We also found that our labeled-site information did not match the known membrane topologies of several proteins (e.g., TOM22 and TOR1AIP1). We think that our labeled-site information may reveal the possibility of dual-membrane topologies of these proteins in live cells. Further investigations might be required to confirm our proposed membrane protein topologies shown in **Figure 15**.

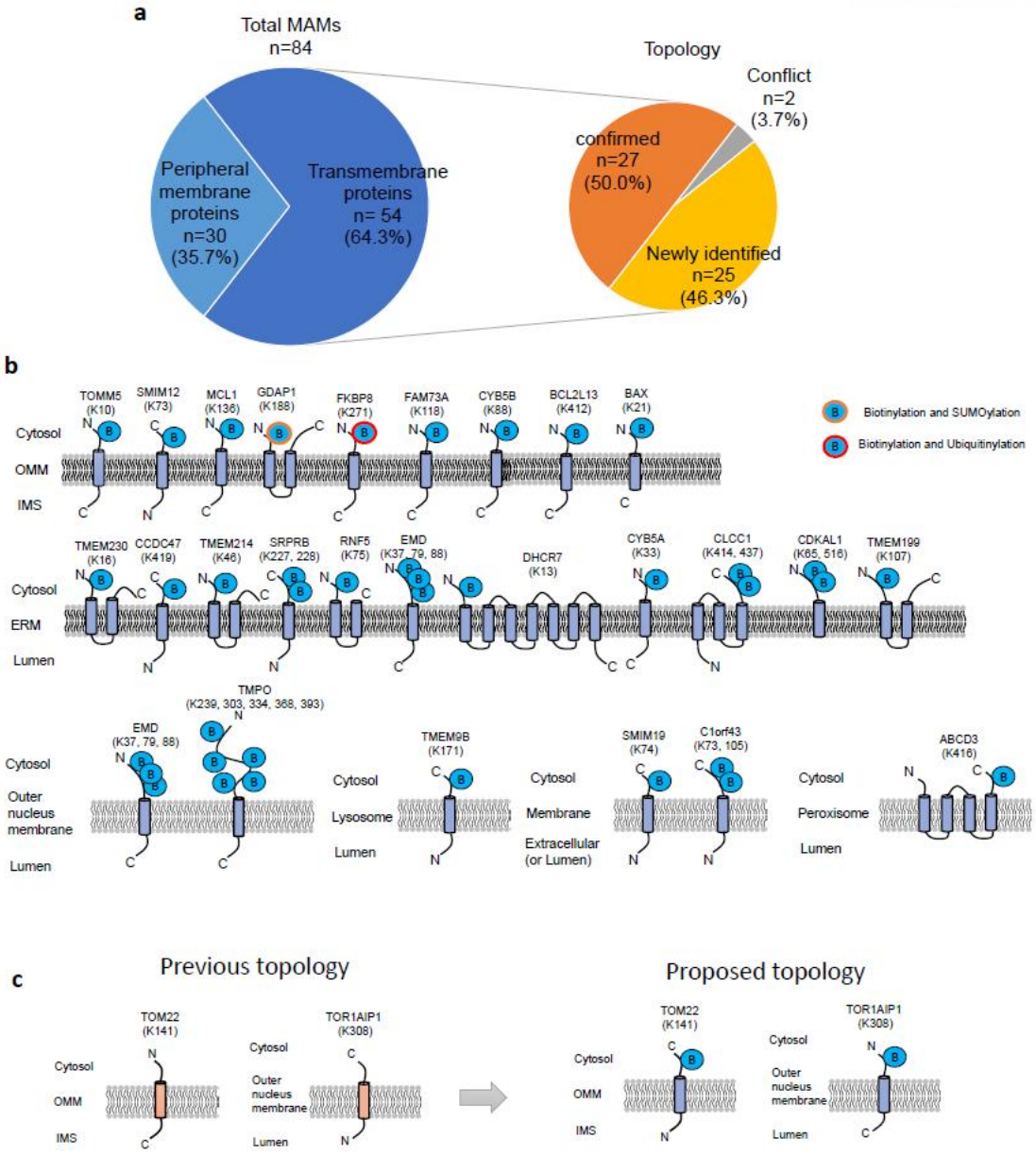


Figure 15. Proposed novel topologies of 27 proteins based on labeled peptides by MCS-ID. **a.** Distribution of labeled peptides of total 84 MAMs and states in topology of 54 transmembrane (TM) proteins. Of the 54 TM proteins, half are correlated with our results and 25 proteins are newly identified in this study because no topology information is available until now. Only 2 topologies of proteins (TOMM22, TOP1AIP1) are conflict with our results. **b.** Schematic representation of 25 novel topologies of proteins. **c.** Schematic representation of 2 conflict topologies.

Ⅴ. Conclusion

Here, we report a split-pBirA system as a sensitive and specific tool for detecting and identifying organelle contacts, especially at the MAM. In contrast to previous research regarding MAM identification, our method provides selective and reliable results, for the first time, to the best of our knowledge. Our method should be valuable in a wide range of MAM-related biological and biomedical research fields.

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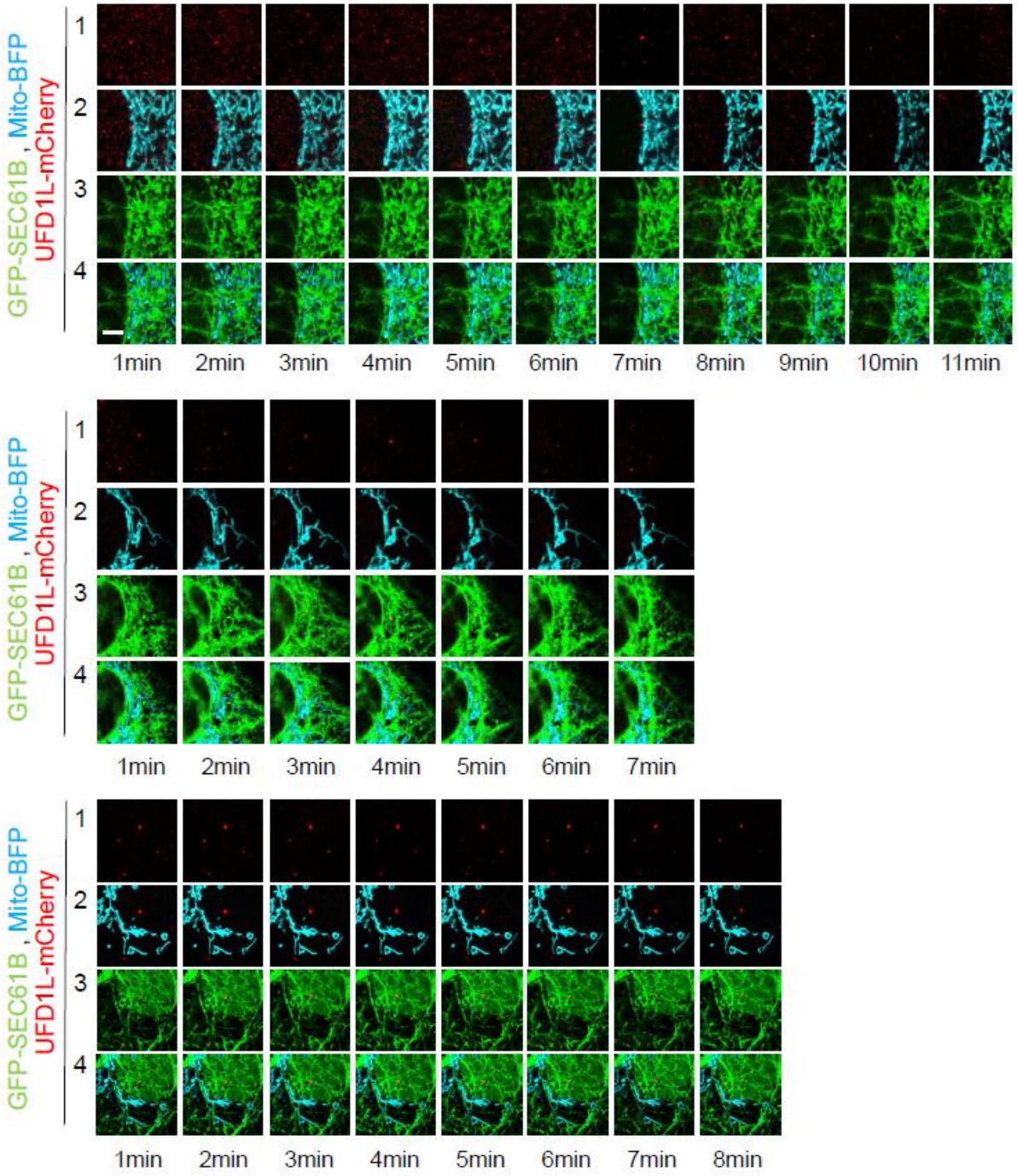
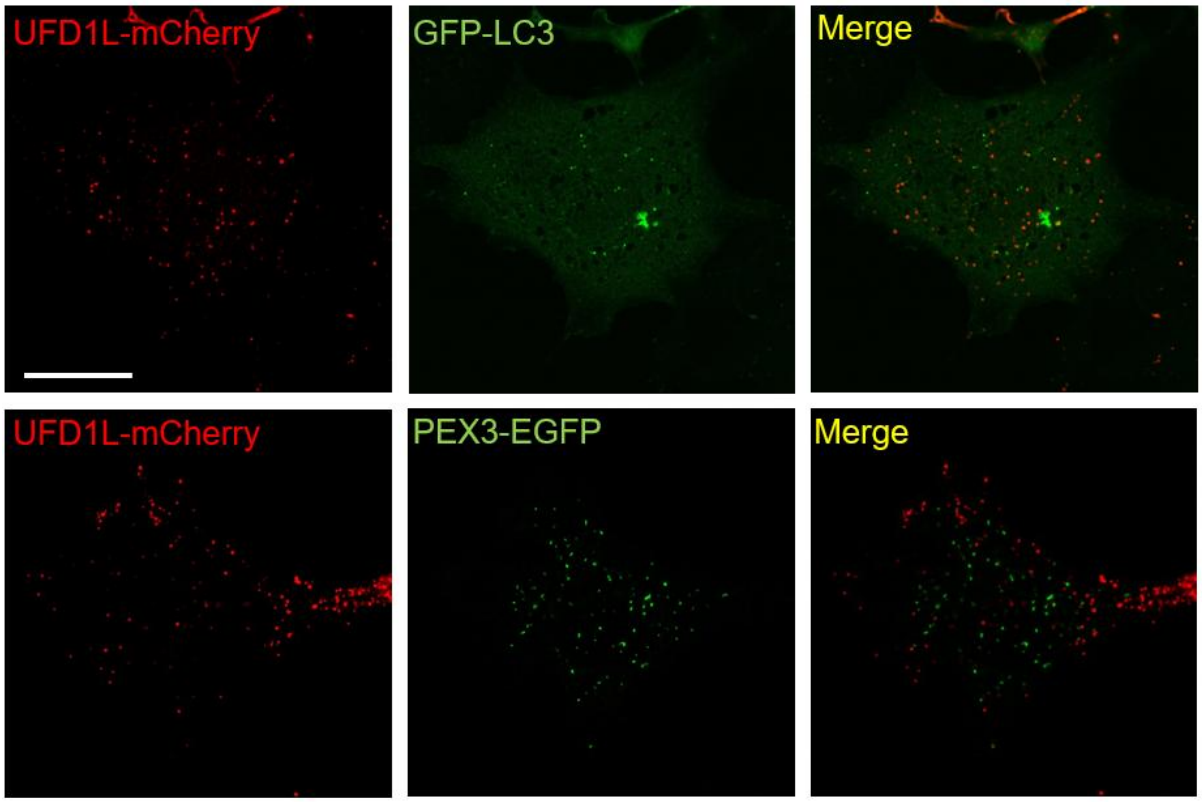
Supplementary Figures



Supplementary Figure 1. Dynamics of UFD1L-mCherry dots with ER, Mito markers. Different sets of live cell images for UFD1L-mCherry dots formation. Distances from mitochondria and ER were calculated and shown in **Figure 12d.** Scale bar, 2um.



Supplementary Figure 2. Co-localization of UFD1L-mCherry dots and lysosome(GFP-LC3), peroxisome(PEX3-EGFP) markers.

Localization of UFD1L-mCherry dots correlated with lysosome marker(GFP-LC3) under starvation condition. Co-localization of UFD1L-mCherry dots with peroxisome marker (PEX3-EGFP) shown in less correlation. Scale bar, 20um.

Ⅶ. Appendix

Appendix A. B-factor information of biotin ligase crystal structure (PDB: 1HXD).

	# of Atom	Chain Identifier	Amino Acid	Amino Acid Position	B-factor
ATOM	2	CA	ASN	4	85.31
ATOM	10	CA	THR	5	50.44
ATOM	17	CA	VAL	6	39.17
ATOM	24	CA	PRO	7	17.87
ATOM	31	CA	LEU	8	33.33
ATOM	39	CA	LYS	9	40.89
ATOM	48	CA	LEU	10	24.72
ATOM	56	CA	ILE	11	23.58
ATOM	64	CA	ALA	12	27.56
ATOM	69	CA	LEU	13	27.84
ATOM	77	CA	LEU	14	27.24
ATOM	85	CA	ALA	15	31.74
ATOM	90	CA	ASN	16	42.33
ATOM	98	CA	GLY	17	46.86
ATOM	102	CA	GLU	18	31.96
ATOM	111	CA	PHE	19	45.28
ATOM	122	CA	HIS	20	21.78
ATOM	132	CA	SER	21	31.54
ATOM	138	CA	GLY	22	41.62
ATOM	142	CA	GLU	23	55.28
ATOM	151	CA	GLN	24	39.31
ATOM	160	CA	LEU	25	35.4
ATOM	168	CA	GLY	26	50.78
ATOM	172	CA	GLU	27	55.79
ATOM	181	CA	THR	28	60.15
ATOM	188	CA	LEU	29	39.86
ATOM	196	CA	GLY	30	63.82
ATOM	200	CA	MET	31	77.69
ATOM	208	CA	SER	32	56.33
ATOM	214	CA	ARG	33	35.25
ATOM	225	CA	ALA	34	24.44
ATOM	230	CA	ALA	35	35.75
ATOM	235	CA	ILE	36	27.46

ATOM	243	CA	ASN	37	19
ATOM	251	CA	LYS	38	43.74
ATOM	260	CA	HIS	39	35.21
ATOM	270	CA	ILE	40	33.87
ATOM	278	CA	GLN	41	46.21
ATOM	287	CA	THR	42	30.28
ATOM	294	CA	LEU	43	25.02
ATOM	302	CA	ARG	44	39.16
ATOM	313	CA	ASP	45	53.5
ATOM	321	CA	TRP	46	32.78
ATOM	335	CA	GLY	47	52.07
ATOM	339	CA	VAL	48	45
ATOM	346	CA	ASP	49	47.47
ATOM	354	CA	VAL	50	40.23
ATOM	361	CA	PHE	51	34.27
ATOM	372	CA	THR	52	22.35
ATOM	379	CA	VAL	53	22.78
ATOM	386	CA	PRO	54	31.69
ATOM	393	CA	GLY	55	21.49
ATOM	397	CA	LYS	56	24.32
ATOM	406	CA	GLY	57	30.52
ATOM	410	CA	TYR	58	19.12
ATOM	422	CA	SER	59	35.03
ATOM	428	CA	LEU	60	40.3
ATOM	436	CA	PRO	61	55.74
ATOM	443	CA	GLU	62	72.51
ATOM	452	CA	PRO	63	58.36
ATOM	459	CA	ILE	64	50.86
ATOM	467	CA	GLN	65	49.64
ATOM	476	CA	LEU	66	24.14
ATOM	484	CA	LEU	67	15.75
ATOM	492	CA	ASN	68	26.68
ATOM	500	CA	ALA	69	15.59
ATOM	505	CA	LYS	70	28.92
ATOM	514	CA	GLN	71	17.98
ATOM	523	CA	ILE	72	11.6
ATOM	531	CA	LEU	73	38.36
ATOM	539	CA	GLY	74	36.99
ATOM	543	CA	GLN	75	36.23
ATOM	552	CA	LEU	76	62.28

ATOM	560	CA	ASP	77	85.88
ATOM	568	CA	GLY	78	97.23
ATOM	572	CA	GLY	79	71.15
ATOM	576	CA	SER	80	26.09
ATOM	582	CA	VAL	81	22.77
ATOM	589	CA	ALA	82	21.37
ATOM	594	CA	VAL	83	25.84
ATOM	601	CA	LEU	84	29.07
ATOM	609	CA	PRO	85	26.55
ATOM	616	CA	VAL	86	19.89
ATOM	623	CA	ILE	87	26.52
ATOM	631	CA	ASP	88	15.68
ATOM	639	CA	SER	89	18.5
ATOM	645	CA	THR	90	34.78
ATOM	652	CA	ASN	91	24.33
ATOM	660	CA	GLN	92	26.17
ATOM	669	CA	TYR	93	18.34
ATOM	681	CA	LEU	94	23.33
ATOM	689	CA	LEU	95	25.56
ATOM	697	CA	ASP	96	32.53
ATOM	705	CA	ARG	97	16
ATOM	716	CA	ILE	98	35.85
ATOM	724	CA	GLY	99	42.99
ATOM	728	CA	GLU	100	23.57
ATOM	737	CA	LEU	101	21.05
ATOM	745	CA	LYS	102	22.69
ATOM	754	CA	SER	103	15.77
ATOM	760	CA	GLY	104	22.67
ATOM	764	CA	ASP	105	9.69
ATOM	772	CA	ALA	106	12.4
ATOM	777	CA	CYS	107	31.14
ATOM	783	CA	ILE	108	16.94
ATOM	791	CA	ALA	109	19.04
ATOM	796	CA	GLU	110	17.99
ATOM	805	CA	TYR	111	10.15
ATOM	817	CA	GLN	112	10.44
ATOM	826	CA	GLN	113	23.47
ATOM	835	CA	ALA	114	18.22
ATOM	840	CA	GLY	115	12.32
ATOM	844	CA	ARG	116	22.28

ATOM	855	CA	GLY	117	17.38
ATOM	859	CA	ARG	118	21.17
ATOM	870	CA	ARG	119	47.08
ATOM	881	CA	GLY	120	38.35
ATOM	885	CA	ARG	121	34.58
ATOM	896	CA	LYS	122	30.08
ATOM	905	CA	TRP	123	18.78
ATOM	919	CA	PHE	124	24.09
ATOM	930	CA	SER	125	29.97
ATOM	936	CA	PRO	126	31.01
ATOM	943	CA	PHE	127	23.86
ATOM	954	CA	GLY	128	16.02
ATOM	958	CA	ALA	129	16.21
ATOM	963	CA	ASN	130	24.51
ATOM	971	CA	LEU	131	18.56
ATOM	979	CA	TYR	132	13.4
ATOM	991	CA	LEU	133	13.3
ATOM	999	CA	SER	134	19.71
ATOM	1005	CA	MET	135	16.41
ATOM	1013	CA	PHE	136	8.46
ATOM	1024	CA	TRP	137	14.99
ATOM	1038	CA	ARG	138	31.1
ATOM	1049	CA	LEU	139	31.04
ATOM	1057	CA	GLU	140	62.49
ATOM	1066	CA	GLN	141	83.28
ATOM	1075	CA	GLY	142	79.45
ATOM	1079	CA	PRO	143	85.17
ATOM	1086	CA	ALA	144	87.01
ATOM	1091	CA	ALA	145	80.58
ATOM	1096	CA	ALA	146	70.59
ATOM	1101	CA	ILE	147	61.42
ATOM	1109	CA	GLY	148	50.61
ATOM	1113	CA	LEU	149	33.15
ATOM	1121	CA	SER	150	23.23
ATOM	1127	CA	LEU	151	30.92
ATOM	1135	CA	VAL	152	16.46
ATOM	1142	CA	ILE	153	13.37
ATOM	1150	CA	GLY	154	10.42
ATOM	1154	CA	ILE	155	20.73
ATOM	1162	CA	VAL	156	22.34

ATOM	1169	CA	MET	157	22.69
ATOM	1177	CA	ALA	158	11.55
ATOM	1182	CA	GLU	159	16.83
ATOM	1191	CA	VAL	160	22.38
ATOM	1198	CA	LEU	161	22.93
ATOM	1206	CA	ARG	162	19.36
ATOM	1217	CA	LYS	163	34.27
ATOM	1226	CA	LEU	164	23.47
ATOM	1234	CA	GLY	165	31.45
ATOM	1238	CA	ALA	166	46.04
ATOM	1243	CA	ASP	167	55.86
ATOM	1251	CA	LYS	168	29.56
ATOM	1260	CA	VAL	169	20.98
ATOM	1267	CA	ARG	170	25.38
ATOM	1278	CA	VAL	171	29.9
ATOM	1285	CA	LYS	172	31.31
ATOM	1294	CA	TRP	173	36.34
ATOM	1308	CA	PRO	174	39.01
ATOM	1315	CA	ASN	175	41.53
ATOM	1323	CA	ASP	176	25.56
ATOM	1331	CA	LEU	177	13.37
ATOM	1339	CA	TYR	178	16.54
ATOM	1351	CA	LEU	179	24.64
ATOM	1359	CA	GLN	180	27.38
ATOM	1368	CA	ASP	181	16.36
ATOM	1376	CA	ARG	182	18.18
ATOM	1387	CA	LYS	183	19.35
ATOM	1396	CA	LEU	184	16.82
ATOM	1404	CA	ALA	185	11.61
ATOM	1409	CA	GLY	186	7.45
ATOM	1413	CA	ILE	187	11.22
ATOM	1421	CA	LEU	188	19.33
ATOM	1429	CA	VAL	189	17.09
ATOM	1436	CA	GLU	190	28.76
ATOM	1445	CA	LEU	191	32.89
ATOM	1453	CA	THR	192	25.62
ATOM	1460	CA	GLY	193	40.55
ATOM	1464	CA	LYS	194	29.31
ATOM	1473	CA	THR	195	46.91
ATOM	1480	CA	GLY	196	52.4

ATOM	1484	CA	ASP	197	47.41
ATOM	1492	CA	ALA	198	30.19
ATOM	1497	CA	ALA	199	11.77
ATOM	1502	CA	GLN	200	22.92
ATOM	1511	CA	ILE	201	8.04
ATOM	1519	CA	VAL	202	15.9
ATOM	1526	CA	ILE	203	33.52
ATOM	1534	CA	GLY	204	14.34
ATOM	1538	CA	ALA	205	23.34
ATOM	1543	CA	GLY	206	26.03
ATOM	1547	CA	ILE	207	19.21
ATOM	1555	CA	ASN	208	19.5
ATOM	1563	CA	MET	209	18.16
ATOM	1571	CA	ALA	210	35.47
ATOM	1576	CA	MET	211	73
ATOM	1584	CA	GLN	221	89.59
ATOM	1593	CA	GLY	222	71.7
ATOM	1597	CA	TRP	223	34.03
ATOM	1611	CA	ILE	224	20.9
ATOM	1619	CA	THR	225	11.45
ATOM	1626	CA	LEU	226	15.83
ATOM	1634	CA	GLN	227	27.52
ATOM	1643	CA	GLU	228	17.82
ATOM	1652	CA	ALA	229	17.35
ATOM	1657	CA	GLY	230	18.2
ATOM	1661	CA	ILE	231	13.64
ATOM	1669	CA	ASN	232	24.89
ATOM	1677	CA	LEU	233	21.08
ATOM	1685	CA	ASP	234	14.51
ATOM	1693	CA	ARG	235	25.79
ATOM	1704	CA	ASN	236	12.05
ATOM	1712	CA	THR	237	20.96
ATOM	1719	CA	LEU	238	24.34
ATOM	1727	CA	ALA	239	19.5
ATOM	1732	CA	ALA	240	18.54
ATOM	1737	CA	MET	241	25.95
ATOM	1745	CA	LEU	242	15.03
ATOM	1753	CA	ILE	243	16.89
ATOM	1761	CA	ARG	244	21.53
ATOM	1772	CA	GLU	245	14.62

ATOM	1781	CA	LEU	246	19.27
ATOM	1789	CA	ARG	247	10.98
ATOM	1800	CA	ALA	248	33.53
ATOM	1805	CA	ALA	249	33.76
ATOM	1810	CA	LEU	250	33.68
ATOM	1818	CA	GLU	251	18.39
ATOM	1827	CA	LEU	252	55.51
ATOM	1835	CA	PHE	253	39.12
ATOM	1846	CA	GLU	254	28.8
ATOM	1855	CA	GLN	255	45.78
ATOM	1864	CA	GLU	256	47.92
ATOM	1873	CA	GLY	257	35.12
ATOM	1877	CA	LEU	258	45.84
ATOM	1885	CA	ALA	259	37.24
ATOM	1890	CA	PRO	260	45.32
ATOM	1897	CA	TYR	261	40.59
ATOM	1909	CA	LEU	262	41.3
ATOM	1917	CA	SER	263	37.53
ATOM	1923	CA	ARG	264	50.57
ATOM	1934	CA	TRP	265	26.02
ATOM	1948	CA	GLU	266	33.11
ATOM	1957	CA	LYS	267	23.63
ATOM	1966	CA	LEU	268	9.25
ATOM	1974	CA	ASP	269	19.55
ATOM	1982	CA	ASN	270	21.43
ATOM	1990	CA	PHE	271	32.87
ATOM	2001	CA	ILE	272	30.48
ATOM	2009	CA	ASN	273	22.13
ATOM	2017	CA	ARG	274	32.34
ATOM	2028	CA	PRO	275	52.76
ATOM	2035	CA	VAL	276	55.34
ATOM	2042	CA	LYS	277	51.12
ATOM	2051	CA	LEU	278	48.09
ATOM	2059	CA	ILE	279	77.9
ATOM	2067	CA	ILE	280	98.13
ATOM	2075	CA	GLY	281	92.61
ATOM	2079	CA	ASP	282	95.7
ATOM	2087	CA	LYS	283	95.81
ATOM	2096	CA	GLU	284	97.2
ATOM	2105	CA	ILE	285	82.68

ATOM	2113	CA	PHE	286	86.59
ATOM	2124	CA	GLY	287	82.62
ATOM	2128	CA	ILE	288	51.92
ATOM	2136	CA	SER	289	37.6
ATOM	2142	CA	ARG	290	28.13
ATOM	2153	CA	GLY	291	23.45
ATOM	2157	CA	ILE	292	40.5
ATOM	2165	CA	ASP	293	55.34
ATOM	2173	CA	LYS	294	55.51
ATOM	2182	CA	GLN	295	61.6
ATOM	2191	CA	GLY	296	35.56
ATOM	2195	CA	ALA	297	30.91
ATOM	2200	CA	LEU	298	18.34
ATOM	2208	CA	LEU	299	39.73
ATOM	2216	CA	LEU	300	43.06
ATOM	2224	CA	GLU	301	41.56
ATOM	2233	CA	GLN	302	53.36
ATOM	2242	CA	ASP	303	65.73
ATOM	2250	CA	GLY	304	41.55
ATOM	2254	CA	ILE	305	36.25
ATOM	2262	CA	ILE	306	42.95
ATOM	2270	CA	LYS	307	49.27
ATOM	2279	CA	PRO	308	53.68
ATOM	2286	CA	TRP	309	83.49
ATOM	2300	CA	MET	310	80.01
ATOM	2308	CA	GLY	311	84.37
ATOM	2312	CA	GLY	312	94.04
ATOM	2316	CA	GLU	313	98.34
ATOM	2325	CA	ILE	314	72.42
ATOM	2333	CA	SER	315	58.69
ATOM	2339	CA	LEU	316	55.63
ATOM	2347	CA	ARG	317	94.07

Appendix B. Summary of MAM list revealed by MCS-ID for 12hrs labeling.

			Relative PSM							
UniProt	Entrez ID	Gene Name	MAM normal	MAM star	ERM normal	ERM star	OMM normal	OMM star	EGFP normal	EGFP star
P60468	10952	SEC61B	5.2055	4.7233	0.9073	0.8634	0.0000	0.1213	0.1261	0.1232
Q96RQ3	56922	MCCC1	5.0685	5.6680	0.6048	0.2093	0.2433	0.5458	0.0000	0.2465
P42167	7112	TMPO	3.4247	3.9136	3.5282	2.4594	0.3244	0.3032	0.3783	0.6778
P50402	2010	EMD	3.2877	3.9136	2.5202	1.8577	0.0000	0.0000	0.0000	0.1848
P51648	224	ALDH3A2	3.1507	2.9690	1.2097	1.4914	1.5410	1.2735	0.0000	0.1848
P05165	5095	PCCA	2.8767	2.2942	0.0000	0.0523	0.1622	0.2426	0.0000	0.0000
Q15388	9804	TOMM20	2.3288	1.7544	0.0000	0.0000	1.4599	1.3948	0.0000	0.0000
O95292	9217	VAPB	2.0548	1.6194	1.1593	1.0466	0.0000	0.0000	0.0000	0.1232
Q14739	3930	LBR	1.9178	2.1592	1.5121	1.4652	0.0000	0.0000	0.0000	0.2465
Q969Z3	54996	MARC2	1.9178	1.8893	0.0000	0.0000	0.6488	0.5458	0.0000	0.0000
Q9BWH2	65991	FUNDC2	1.9178	1.4845	0.0000	0.0000	0.4055	0.3639	0.0000	0.0000
O15498	10652	YKT6	1.7808	2.0243	1.2097	0.6803	1.1354	1.3341	0.0000	0.0000
Q8N4H5	401505	TOMM5	1.7808	1.3495	0.0000	0.0000	0.2433	0.2426	0.0000	0.0000
Q9H3N1	81542	TMX1	1.7808	1.3495	0.6552	0.4186	0.0000	0.0000	0.0000	0.0000
O15155	10282	BET1	1.6438	2.0243	0.9073	0.5756	0.0000	0.0000	0.0000	0.0000
Q8N511	147007	TMEM199	1.6438	2.4291	0.3528	0.3663	0.0000	0.0000	0.0000	0.1232
Q9NX40	54940	OCIAD1	1.6438	1.4845	0.0000	0.0523	2.8386	2.0012	0.0000	0.0000
Q9NZ45	55847	CISD1	1.5068	1.4845	0.0000	0.0523	0.9732	0.6671	0.1261	0.0000
Q14318	23770	FKBP8	1.3699	0.6748	0.3528	0.4186	1.2976	1.3948	0.0000	0.0000
P54652	3306	HSPA2	1.0959	1.2146	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Q96A57	29058	TMEM230	1.0959	1.3495	0.2520	0.2878	0.0000	0.0000	0.0000	0.0000
Q9BWL3	25912	C1orf43	1.0959	1.0796	0.1512	0.1570	0.0000	0.0000	0.0000	0.0000
Q9Y6I9	51368	TEX264	1.0959	1.3495	0.5544	0.3401	0.0000	0.0000	0.0000	0.0000
P28288	5825	ABCD3	0.9589	1.4845	0.1512	0.0785	1.1354	1.2735	0.0000	0.0000
Q5HYI8	285282	RABL3	0.9589	0.8097	0.3024	0.1832	0.0000	0.0000	0.0000	0.0000
Q8N4V1	93380	MMGT1	0.9589	1.2146	1.5121	0.7064	0.0000	0.0000	0.0000	0.0000
Q9Y385	51465	UBE2J1	0.9589	0.5398	0.2520	0.2616	0.0000	0.0000	0.0000	0.1232
Q07812	581	BAX	0.8219	0.6748	0.1008	0.0523	0.2433	0.2426	0.0000	0.0000
Q96A33	57003	CCDC47	0.8219	0.8097	1.0081	0.2878	0.0000	0.0000	0.0000	0.0000
Q96HY6	65992	DDRGK1	0.8219	0.9447	0.5544	0.4186	0.0000	0.0000	0.0000	0.0000
Q99640	9088	PKMYT1	0.8219	0.0000	0.3528	0.2355	0.0000	0.0000	0.0000	0.0000
Q9NQ34	56674	TMEM9B	0.8219	0.0000	0.2520	0.2093	0.0000	0.0000	0.0000	0.0000
O00264	10857	PGRMC1	0.6849	0.5398	0.6048	0.3925	0.0000	0.0000	0.0000	0.0000
O43169	80777	CYB5B	0.6849	0.6748	0.0000	0.1047	0.5677	0.4245	0.0000	0.0000

O75915	10550	ARL6IP5	0.6849	0.6748	0.2520	0.1570	0.0000	0.0000	0.0000	0.0000
P46109	1399	CRKL	0.6849	1.2146	1.0585	0.5756	1.4599	1.0916	0.0000	0.5545
Q96E16	114926	SMIM19	0.6849	0.9447	0.4536	0.4710	0.0000	0.0000	0.0000	0.0000
Q96S66	23155	CLCC1	0.6849	0.8097	1.0585	0.6279	0.0000	0.0000	0.0000	0.0000
O75396	9554	SEC22B	0.5479	0.8097	0.1512	0.1308	0.0000	0.0000	0.0000	0.0000
P00167	1528	CYB5A	0.5479	0.5398	0.7560	0.3140	0.5677	0.4851	0.0000	0.0000
P05556	3688	ITGB1	0.5479	0.0000	0.3024	0.2355	0.0000	0.0000	0.0000	0.0000
Q5VV42	54901	CDKAL1	0.5479	0.5398	0.7560	0.6018	0.0000	0.0000	0.0000	0.0000
Q96EX1	113444	SMIM12	0.5479	0.4049	0.1008	0.1832	0.1622	0.1819	0.0000	0.0000
Q9NVH0	55218	EXD2	0.5479	0.6748	0.0000	0.0523	0.4055	0.4245	0.0000	0.0000
Q9P0T7	252839	TMEM9	0.5479	0.5398	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
Q9UBM7	1717	DHCR7	0.5479	0.4049	0.2520	0.2355	0.0000	0.0000	0.0000	0.0000
Q9Y2W6	11022	TDRKH	0.5479	0.5398	0.0000	0.0000	0.8921	1.0309	0.0000	0.0000
Q9Y5M8	58477	SRPRB	0.5479	0.6748	0.2520	0.2093	0.0000	0.0000	0.0000	0.0000
O00400	9197	SLC33A1	0.4110	0.0000	0.5040	0.2355	0.0000	0.0000	0.0000	0.0000
P14625	7184	HSP90B1	0.4110	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
P43307	6745	SSR1	0.4110	0.6748	0.5040	0.3663	0.0000	0.0000	0.0000	0.0000
Q15005	9789	SPCS2	0.4110	0.5398	0.4536	0.2355	0.0000	0.0000	0.0000	0.0000
Q5HYI7	345778	MTX3	0.4110	0.9447	0.0000	0.0000	0.4866	0.3639	0.0000	0.0000
Q7Z2W4	56829	ZC3HAV1	0.4110	0.8097	1.0081	0.5495	1.6221	1.5161	0.1892	0.0000
Q8TB36	54332	GDAP1	0.4110	0.6748	0.0000	0.0000	0.4055	0.4245	0.0000	0.0000
Q9BXK5	23786	BCL2L13	0.4110	0.0000	0.0000	0.0000	0.8110	0.7884	0.0000	0.0000
Q9HCU5	10113	PREB	0.4110	0.5398	0.1008	0.2878	0.0000	0.0000	0.0000	0.0000
Q9UH92	6945	MLX	0.4110	0.2699	0.0000	0.0000	0.1622	0.1819	0.0000	0.0000
Q9Y394	51635	DHRS7	0.4110	0.6748	0.3024	0.2616	0.0000	0.0000	0.0000	0.0000
O00165	10456	HAX1	0.2740	0.0000	0.0000	0.0523	0.3244	0.0000	0.0000	0.0000
P00918	760	CA2	0.2740	0.4049	0.1008	0.0523	0.0000	0.0000	0.0000	0.1232
P06576	506	ATP5B	0.2740	0.4049	0.0000	0.0000	1.0543	1.2735	0.0000	0.0000
P20340	5870	RAB6A	0.2740	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
P53801	754	PTTG1IP	0.2740	0.2699	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
P84077	375	ARF1	0.2740	0.0000	0.6048	0.2093	0.5677	0.5458	0.1261	0.0000
Q07820	4170	MCL1	0.2740	0.0000	0.2520	0.1308	0.1622	0.1819	0.0000	0.0000
Q86UE4	92140	MTDH	0.2740	0.2699	1.8145	1.7268	0.0000	0.0000	0.0000	0.1232
Q8NAN2	374986	FAM73A	0.2740	0.0000	0.0000	0.0000	0.2433	0.2426	0.0000	0.0000
Q9C0E8	80856	LNP	0.2740	0.5398	0.5544	0.3140	0.0000	0.0000	0.0000	0.0000
Q9NZ43	55850	USE1	0.2740	0.2699	0.4032	0.3663	0.0000	0.0000	0.0000	0.0000
Q9UHB9	6730	SRP68	0.2740	0.2699	0.2016	0.1047	0.1622	0.0000	0.0000	0.0000
Q9Y679	550	AUP1	0.2740	0.0000	0.3024	0.1832	0.0000	0.0000	0.0000	0.0000
Q9Y6X1	27230	SERP1	0.2740	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P11498	5091	PC	2.8767	2.0243	0.5544	0.4448	1.8654	1.6980	1.0719	1.1091

O95721	9342	SNAP29	2.4658	1.8893	1.4617	0.9942	1.5410	1.3341	0.3153	0.4313
P37802	8407	TAGLN2	2.4658	2.1592	0.6552	0.3663	1.0543	0.7277	0.5675	0.7394
O15173	10424	PGRMC2	2.3288	2.4291	0.8065	0.4710	0.3244	0.2426	0.2522	0.1848
Q7Z434	57506	MAVS	2.1918	0.9447	0.1008	0.2616	5.2717	4.9727	0.1892	0.1848
Q9H1E3	64710	NUCKS1	1.6438	1.3495	0.4536	0.3663	1.1354	0.8490	1.5132	1.3555
P46108	1398	CRK	1.2329	1.2146	0.7560	0.5495	1.5410	1.3341	0.3783	0.5545
P46060	5905	RANGAP1	0.8219	0.5398	0.6048	0.4971	0.0000	0.0000	0.6305	0.5545
P55010	1983	EIF5	0.8219	0.4049	0.5040	0.2093	0.1622	0.1819	0.7566	0.7394
P63027	6844	VAMP2	0.8219	0.8097	0.2520	0.1570	0.1622	0.1213	0.1261	0.1232
Q99618	83461	CDCA3	0.8219	0.6748	0.1512	0.1047	0.1622	0.1213	0.1261	0.1232
Q9NZC7	51741	WWOX	0.6849	0.6748	0.1512	0.0785	0.2433	0.1213	0.1892	0.1848
P07737	5216	PFN1	0.5479	0.4049	0.2016	0.1832	0.3244	0.4245	0.3783	0.3081
P49321	4678	NASP	0.4110	0.0000	0.0000	0.0000	0.0000	0.0000	0.3153	0.2465
P49327	2194	FASN	0.4110	0.0000	0.3528	0.1832	0.0000	0.3639	0.6936	0.6778
Q14677	9685	CLINT1	0.4110	0.5398	0.2520	0.4971	2.3520	2.4257	0.6305	0.7394
Q15084	10130	PDIA6	0.4110	0.2699	0.0000	0.0523	0.1622	0.1213	0.1261	0.1232
Q8N6T3	55738	ARFGAP1	0.4110	0.2699	0.3528	0.3401	0.3244	0.6064	0.1892	0.4313
Q96A49	94056	SYAP1	0.4110	0.0000	0.7056	0.4448	0.4866	0.4851	0.2522	0.4313
Q99733	4676	NAP1L4	0.4110	0.0000	0.0000	0.2093	0.2433	0.3639	0.1261	0.1232
Q32P51	144983	HNRNPA1L2	0.2740	0.0000	0.0000	0.0000	0.1622	0.1213	0.1892	0.1848
Q7Z6K5	348110	ARPIN	0.2740	0.0000	0.2016	0.1570	0.0000	0.1213	0.3783	0.2465
Q9H307	5411	PNN	0.2740	0.5398	0.2016	0.0785	0.9732	0.7277	0.8827	0.6161
O14683	9537	TP53I11	0.0000	0.8097	0.2016	0.2093	0.0000	0.0000	0.0000	0.0000
Q5JTV8	26092	TOR1AIP1	0.0000	0.6748	1.3105	0.7849	0.0000	0.0000	0.0000	0.0000
O75787	10159	ATP6AP2	0.0000	0.5398	0.1008	0.0523	0.0000	0.0000	0.0000	0.1232
Q13190	6811	STX5	0.0000	0.5398	0.1008	0.1570	0.0000	0.0000	0.0000	0.0000
Q9GZY8	56947	MFF	0.0000	0.5398	0.0000	0.0000	0.2433	0.3639	0.0000	0.0000
Q6NUQ4	54867	TMEM214	0.0000	0.4049	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q70CQ3	84749	USP30	0.0000	0.4049	0.0000	0.0000	0.5677	0.6064	0.0000	0.0000
P30519	3163	HMOX2	0.0000	0.2699	0.5040	0.2878	0.0000	0.0000	0.0000	0.0000
P57105	55333	SYNJ2BP	0.0000	0.2699	0.0000	0.0000	0.3244	0.3639	0.0000	0.0000
Q8TAA9	81839	VANGL1	0.0000	0.2699	0.2520	0.1308	0.0000	0.0000	0.0000	0.0000
Q92890	7353	UFD1L	0.0000	0.2699	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q99942	6048	RNF5	0.0000	0.2699	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
Q9H089	55341	LSG1	0.0000	0.2699	0.4536	0.2355	0.0000	0.0000	0.0000	0.0000
Q9NS69	56993	TOMM22	0.0000	0.2699	0.0000	0.0000	0.2433	0.3639	0.0000	0.0000
Q9Y4P3	26608	TBL2	0.0000	0.2699	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q9BQ61	79002	C19orf43	0.0000	0.5398	0.2016	0.0785	0.4055	0.4851	0.3153	0.3697
Q14247	2017	CTTN	0.0000	0.4049	1.2097	1.3605	0.9732	1.4554	2.8373	2.2797
Q96NC0	153527	ZMAT2	0.0000	0.4049	0.1008	0.0523	0.3244	0.2426	0.1892	0.1232

Q9NZZ3	51510	CHMP5	0.0000	0.4049	0.3528	0.3401	0.0000	0.0000	0.7566	0.9858
P17844	1655	DDX5	0.0000	0.2699	0.0000	0.0523	0.2433	0.2426	0.1261	0.1232
Q15843	4738	NEDD8	0.0000	0.2699	0.2520	0.1308	0.0000	0.1819	0.1892	0.3081
Q9UEE9	10428	CFDP1	0.0000	0.2699	0.0000	0.0785	0.1622	0.1213	0.3783	0.3697
Q86UP2	3895	KTN1	0.0000	0.0000	1.3609	0.8896	0.0000	0.0000	0.0000	0.0000
Q9P0L0	9218	VAPA	0.0000	0.0000	1.1089	0.9419	0.0000	0.0000	0.0000	0.0000
P84157	439921	MXRA7	0.0000	0.0000	0.9577	1.0204	0.0000	0.0000	0.1261	0.0000
Q13586	6786	STIM1	0.0000	0.0000	0.9577	0.6541	0.0000	0.0000	0.0000	0.0000
Q86XL3	23141	ANKLE2	0.0000	0.0000	0.9073	0.8634	0.0000	0.0000	0.0000	0.0000
Q96AG4	55379	LRRC59	0.0000	0.0000	0.8065	0.4448	0.0000	0.0000	0.0000	0.0000
P51572	10134	BCAP31	0.0000	0.0000	0.6552	0.4710	0.0000	0.0000	0.0000	0.0000
Q969M3	81555	YIPF5	0.0000	0.0000	0.6048	0.2355	0.0000	0.0000	0.0000	0.0000
Q9P2E9	6238	RRBP1	0.0000	0.0000	0.5544	0.4448	0.0000	0.0000	0.0000	0.0000
Q96SK2	84928	TMEM209	0.0000	0.0000	0.5040	0.3663	0.0000	0.0000	0.0000	0.0000
Q9BZF1	114882	OSBPL8	0.0000	0.0000	0.5040	0.2878	0.0000	0.0000	0.0000	0.0000
Q8NEN9	118987	PDZD8	0.0000	0.0000	0.4536	0.3925	0.0000	0.0000	0.0000	0.0000
O95210	8987	STBD1	0.0000	0.0000	0.4032	0.3925	0.0000	0.0000	0.0000	0.0000
P04075	226	ALDOA	0.0000	0.0000	0.4032	0.1047	0.3244	0.2426	0.0000	0.1232
P20700	4001	LMNB1	0.0000	0.0000	0.4032	0.4710	0.0000	0.0000	0.0000	0.0000
P52948	4928	NUP98	0.0000	0.0000	0.4032	0.2616	0.0000	0.1213	0.1261	0.0000
Q15738	50814	NSDHL	0.0000	0.0000	0.4032	0.2355	0.0000	0.0000	0.0000	0.0000
Q92575	23190	UBXN4	0.0000	0.0000	0.4032	0.4186	0.0000	0.1213	0.0000	0.0000
Q9BSJ8	23344	ESYT1	0.0000	0.0000	0.4032	0.3140	0.0000	0.0000	0.0000	0.0000
Q9H910	90861	HN1L	0.0000	0.0000	0.4032	0.3925	0.5677	0.2426	0.6305	0.0000
P42167-2	7112	TMPO	0.0000	0.0000	0.3528	0.2093	0.0000	0.0000	0.0000	0.0000
Q00765	7905	REEP5	0.0000	0.0000	0.3528	0.1832	0.0000	0.0000	0.0000	0.0000
Q9ULK5	57216	VANGL2	0.0000	0.0000	0.3528	0.1832	0.0000	0.0000	0.0000	0.0000
O15027	9919	SEC16A	0.0000	0.0000	0.3024	0.3663	0.0000	0.0000	0.0000	0.0000
O75694	9631	NUP155	0.0000	0.0000	0.3024	0.2616	0.0000	0.1213	0.0000	0.0000
P08240	6734	SRPR	0.0000	0.0000	0.3024	0.1832	0.0000	0.0000	0.0000	0.0000
P35610	6646	SOAT1	0.0000	0.0000	0.3024	0.3925	0.0000	0.0000	0.0000	0.0000
P78536	6868	ADAM17	0.0000	0.0000	0.3024	0.3140	0.0000	0.0000	0.0000	0.0000
Q07065	10970	CKAP4	0.0000	0.0000	0.3024	0.2093	0.0000	0.0000	0.0000	0.0000
Q8TBA6	9950	GOLGA5	0.0000	0.0000	0.3024	0.2093	0.0000	0.0000	0.1892	0.0000
Q96BZ9	128637	TBC1D20	0.0000	0.0000	0.3024	0.2355	0.0000	0.0000	0.0000	0.0000
Q96KC8	64215	DNAJC1	0.0000	0.0000	0.3024	0.2878	0.0000	0.0000	0.0000	0.0000
Q9H3P7	64746	ACBD3	0.0000	0.0000	0.3024	0.3925	0.0000	0.0000	0.0000	0.0000
Q9NVV0	55151	TMEM38B	0.0000	0.0000	0.3024	0.1308	0.0000	0.0000	0.0000	0.0000
Q9P2W9	53407	STX18	0.0000	0.0000	0.3024	0.3925	0.0000	0.0000	0.0000	0.0000
A0FGR8	57488	ESYT2	0.0000	0.0000	0.2520	0.2093	0.0000	0.0000	0.0000	0.0000

O14641	1856	DVL2	0.0000	0.0000	0.2520	0.0000	0.0000	0.0000	0.0000	0.0000
P16435	5447	POR	0.0000	0.0000	0.2520	0.2093	0.0000	0.0000	0.0000	0.0000
P49790	9972	NUP153	0.0000	0.0000	0.2520	0.3140	0.0000	0.0000	0.0000	0.0000
Q12981	662	BNIP1	0.0000	0.0000	0.2520	0.1832	0.0000	0.0000	0.0000	0.0000
Q6ZVM7	146691	TOM1L2	0.0000	0.0000	0.2520	0.0785	0.0000	0.0000	0.0000	0.1848
Q9NP61	26286	ARFGAP3	0.0000	0.0000	0.2520	0.2878	0.1622	0.1819	0.1261	0.0000
Q9NQC3	57142	RTN4	0.0000	0.0000	0.2520	0.2878	0.0000	0.0000	0.0000	0.0000
Q9Y2U8	23592	LEMD3	0.0000	0.0000	0.2520	0.1570	0.0000	0.0000	0.0000	0.0000
Q9Y4P8	26100	WIPI2	0.0000	0.0000	0.2520	0.0000	0.0000	0.0000	0.0000	0.0000
A8CG34	0	POM121C	0.0000	0.0000	0.2016	0.1832	0.0000	0.0000	0.0000	0.0000
O00767	6319	SCD	0.0000	0.0000	0.2016	0.2355	0.0000	0.0000	0.0000	0.0000
O14668	5638	PRRG1	0.0000	0.0000	0.2016	0.1308	0.0000	0.0000	0.0000	0.0000
O43768	2029	ENSA	0.0000	0.0000	0.2016	0.1047	0.1622	0.1819	0.2522	0.0000
O60664	10226	PLIN3	0.0000	0.0000	0.2016	0.2093	0.0000	0.0000	0.3783	0.0000
P00374	1719	DHFR	0.0000	0.0000	0.2016	0.0785	0.0000	0.0000	0.0000	0.0000
P06493	983	CDK1	0.0000	0.0000	0.2016	0.1047	0.0000	0.0000	0.0000	0.0000
P07099	2052	EPHX1	0.0000	0.0000	0.2016	0.1047	0.0000	0.0000	0.0000	0.0000
P27824	821	CANX	0.0000	0.0000	0.2016	0.3925	0.0000	0.0000	0.0000	0.1848
P60842	1973	EIF4A1	0.0000	0.0000	0.2016	0.0523	0.0000	0.0000	0.0000	0.0000
Q13501	8878	SQSTM1	0.0000	0.0000	0.2016	0.1308	0.0000	0.0000	0.1892	0.0000
Q16850	1595	CYP51A1	0.0000	0.0000	0.2016	0.2355	0.0000	0.0000	0.0000	0.0000
Q5JRA6	375056	MIA3	0.0000	0.0000	0.2016	0.3401	0.0000	0.0000	0.0000	0.1232
Q5SQN1	116841	SNAP47	0.0000	0.0000	0.2016	0.2355	0.5677	0.4851	0.0000	0.0000
Q8N5G2	55219	TMEM57	0.0000	0.0000	0.2016	0.2355	0.0000	0.0000	0.0000	0.0000
Q8NDI1	23301	EHBP1	0.0000	0.0000	0.2016	0.1570	0.3244	0.3032	0.0000	0.0000
Q8NF91	23345	SYNE1	0.0000	0.0000	0.2016	0.0523	0.0000	0.0000	0.0000	0.0000
Q8TCT9	81502	HM13	0.0000	0.0000	0.2016	0.1832	0.0000	0.0000	0.0000	0.0000
Q96CS3	23197	FAF2	0.0000	0.0000	0.2016	0.4710	0.1622	0.1213	0.0000	0.0000
Q99653	11261	CHP1	0.0000	0.0000	0.2016	0.1047	0.0000	0.0000	0.0000	0.0000
Q9H6U8	79796	ALG9	0.0000	0.0000	0.2016	0.1047	0.0000	0.0000	0.0000	0.0000
Q9NRY5	10827	FAM114A2	0.0000	0.0000	0.2016	0.2093	0.0000	0.0000	0.0000	0.0000
Q9NYP7	60481	ELOVL5	0.0000	0.0000	0.2016	0.1832	0.0000	0.0000	0.0000	0.0000
Q9UGP8	11231	SEC63	0.0000	0.0000	0.2016	0.3140	0.0000	0.0000	0.0000	0.0000
Q9UHQ9	51706	CYB5R1	0.0000	0.0000	0.2016	0.0785	0.0000	0.0000	0.0000	0.0000
Q9UNK0	9482	STX8	0.0000	0.0000	0.2016	0.2878	0.0000	0.0000	0.0000	0.0000
O00124	7993	UBXN8	0.0000	0.0000	0.1512	0.3401	0.0000	0.0000	0.0000	0.0000
O14908	10755	GIPC1	0.0000	0.0000	0.1512	0.0523	0.0000	0.0000	0.0000	0.0000
O60493	8724	SNX3	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.1892	0.0000
O75379	8674	VAMP4	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.0000	0.0000
O75792	10535	RNASEH2A	0.0000	0.0000	0.1512	0.0000	0.0000	0.0000	0.1892	0.0000

O75844	10269	ZMPSTE24	0.0000	0.0000	0.1512	0.2616	0.0000	0.0000	0.0000	0.0000
O75845	6309	SC5D	0.0000	0.0000	0.1512	0.1308	0.0000	0.0000	0.0000	0.0000
O94874	23376	UFL1	0.0000	0.0000	0.1512	0.0523	0.0000	0.0000	0.0000	0.0000
O95551	51567	TDP2	0.0000	0.0000	0.1512	0.0523	0.0000	0.1819	0.1892	0.0000
O95873	57827	C6orf47	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.0000	0.0000
P15311	7430	EZR	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.0000	0.1232
P49023	5829	PXN	0.0000	0.0000	0.1512	0.0523	0.0000	0.0000	0.0000	0.0000
P49069	819	CAMLG	0.0000	0.0000	0.1512	0.2093	0.0000	0.0000	0.0000	0.0000
P51617	3654	IRAK1	0.0000	0.0000	0.1512	0.1308	0.0000	0.0000	0.0000	0.0000
P52565	396	ARHGDIA	0.0000	0.0000	0.1512	0.0785	0.0000	0.0000	0.0000	0.1848
P62330	382	ARF6	0.0000	0.0000	0.1512	0.1047	0.0000	0.1213	0.0000	0.0000
Q07960	392	ARHGAP1	0.0000	0.0000	0.1512	0.2878	0.0000	0.0000	0.0000	0.0000
Q13263	10155	TRIM28	0.0000	0.0000	0.1512	0.1570	0.2433	0.0000	0.0000	0.7394
Q15208	11329	STK38	0.0000	0.0000	0.1512	0.0523	0.1622	0.1213	0.1261	0.0000
Q15366	5094	PCBP2	0.0000	0.0000	0.1512	0.0523	0.1622	0.2426	0.1261	0.0000
Q15758	6510	SLC1A5	0.0000	0.0000	0.1512	0.2093	0.0000	0.0000	0.0000	0.0000
Q16799	6252	RTN1	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.0000	0.0000
Q4KMQ2	196527	ANO6	0.0000	0.0000	0.1512	0.0785	0.0000	0.0000	0.0000	0.0000
Q53FV1	29095	ORMDL2	0.0000	0.0000	0.1512	0.0785	0.0000	0.0000	0.0000	0.0000
Q6P5Z2	29941	PKN3	0.0000	0.0000	0.1512	0.0785	0.0000	0.0000	0.0000	0.0000
Q6PL24	283578	TMED8	0.0000	0.0000	0.1512	0.0785	0.0000	0.0000	0.0000	0.0000
Q8IWZ8	57794	SUGP1	0.0000	0.0000	0.1512	0.0523	0.2433	0.2426	0.3153	0.0000
Q8N5K1	493856	CISD2	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.0000	0.0000
Q8NDI1-2	23301	EHBP1	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.0000	0.0000
Q8NFQ8	163590	TOR1AIP2	0.0000	0.0000	0.1512	0.2878	0.0000	0.0000	0.0000	0.0000
Q8WUM0	55746	NUP133	0.0000	0.0000	0.1512	0.1832	0.0000	0.0000	0.0000	0.0000
Q8WUX9	91782	CHMP7	0.0000	0.0000	0.1512	0.2093	0.0000	0.0000	0.0000	0.0000
Q96GC9	81671	VMP1	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.0000	0.0000
Q96HA1	9883	POM121	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.0000	0.0000
Q96HR9	92840	REEP6	0.0000	0.0000	0.1512	0.0523	0.0000	0.0000	0.0000	0.0000
Q9BTX1	55706	NDC1	0.0000	0.0000	0.1512	0.2878	0.0000	0.0000	0.0000	0.0000
Q9HBM0	55591	VEZT	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.0000	0.0000
Q9HDC5	56704	JPH1	0.0000	0.0000	0.1512	0.2093	0.0000	0.0000	0.0000	0.0000
Q9NRG9	8086	AAAS	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.0000	0.0000
Q9NYM9	51272	BET1L	0.0000	0.0000	0.1512	0.1047	0.0000	0.0000	0.0000	0.0000
Q9NZJ5	9451	EIF2AK3	0.0000	0.0000	0.1512	0.2355	0.0000	0.0000	0.0000	0.0000
Q9P0L0-2	9218	VAPA	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.0000	0.0000
Q9UBC2-3	58513	EPS15L1	0.0000	0.0000	0.1512	0.0523	0.0000	0.0000	0.0000	0.0000
Q9UGP4	8994	LIMD1	0.0000	0.0000	0.1512	0.1308	0.1622	0.1213	0.0000	0.0000
Q9Y2H6	22862	FNDC3A	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.0000	0.0000

A2RRP1	51594	NBAS	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
O14639	3983	ABLIM1	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.1232
O14681	9538	EI24	0.0000	0.0000	0.1008	0.1832	0.0000	0.0000	0.0000	0.0000
O14964	9146	HGS	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.1232
O14967	1047	CLGN	0.0000	0.0000	0.1008	0.1308	0.0000	0.0000	0.0000	0.0000
O43426	8867	SYNJ1	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
O60831	11230	PRAF2	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
O76094	6731	SRP72	0.0000	0.0000	0.1008	0.1570	0.0000	0.0000	0.0000	0.0000
O94929	22885	ABLIM3	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.1232
O95372	11313	LYPLA2	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
O95433	10598	AHSA1	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
O95905	11319	ECD	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
P04035	3156	HMGCR	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
P05023	476	ATP1A1	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
P05783	3875	KRT18	0.0000	0.0000	0.1008	0.0523	0.1622	0.1213	0.0000	0.1848
P09601	3162	HMOX1	0.0000	0.0000	0.1008	0.1308	0.0000	0.0000	0.0000	0.0000
P17706	5771	PTPN2	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
P18031	5770	PTPN1	0.0000	0.0000	0.1008	0.3663	0.4055	0.2426	0.0000	0.0000
P35241	5962	RDX	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
P46379	7917	BAG6	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
P49674	1.03E+08	CSNK1E	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
P61619	29927	SEC61A1	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
P61956	6613	SUMO2	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
P61970	10204	NUTF2	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
P62820	5861	RAB1A	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
P84157-2	439921	MXRA7	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q01813	5214	PFKP	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q03252	84823	LMNB2	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q12982	663	BNIP2	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q13151	10949	HNRNPA0	0.0000	0.0000	0.1008	0.0000	0.0000	0.1213	0.0000	0.0000
Q13371	5082	PDCL	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q14126	1829	DSG2	0.0000	0.0000	0.1008	0.2093	0.0000	0.0000	0.0000	0.0000
Q15056	7458	EIF4H	0.0000	0.0000	0.1008	0.1308	0.0000	0.0000	0.0000	0.1232
Q58FG1	0	HSP90AA4P	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q5BJH7	90522	YIF1B	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q5T9L3	79971	WLS	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q629K1	286144	TRIQK	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q6P1M0	10999	SLC27A4	0.0000	0.0000	0.1008	0.1308	0.0000	0.0000	0.0000	0.0000
Q7L5N7	54947	LPCAT2	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q7Z3D4	116068	LYSMD3	0.0000	0.0000	0.1008	0.1570	0.0000	0.0000	0.0000	0.0000

Q86YA3	55345	ZGRF1	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q8N183	91942	NDUFAF2	0.0000	0.0000	0.1008	0.2093	0.0000	0.0000	0.0000	0.0000
Q8N6H7	84364	ARFGAP2	0.0000	0.0000	0.1008	0.2093	0.0000	0.0000	0.0000	0.0000
Q8N6R1	387923	SERP2	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q8NBT2	147841	SPC24	0.0000	0.0000	0.1008	0.1570	0.1622	0.0000	0.0000	0.0000
Q8TC07	64786	TBC1D15	0.0000	0.0000	0.1008	0.0000	0.4055	0.2426	0.1892	0.0000
Q8TCD1	497661	C18orf32	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q8TCJ2	201595	STT3B	0.0000	0.0000	0.1008	0.1570	0.0000	0.0000	0.0000	0.0000
Q8WVM8	23256	SCFD1	0.0000	0.0000	0.1008	0.1832	0.0000	0.0000	0.0000	0.0000
Q92574	7248	TSC1	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q92667	8165	AKAP1	0.0000	0.0000	0.1008	0.0000	1.8654	1.5161	0.0000	0.0000
Q96EA4	54908	SPDL1	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q96GQ5	64755	C16orf58	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q96JJ7	54495	TMX3	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q96KA5	81037	CLPTM1L	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q96RD7	24145	PANX1	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q99614	7265	TTC1	0.0000	0.0000	0.1008	0.0000	0.3244	0.2426	0.0000	0.0000
Q9BQE5	23780	APOL2	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q9BV19	79078	C1orf50	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q9BW60	64834	ELOVL1	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q9H2M9	25782	RAB3GAP2	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
Q9H425	84886	C1orf198	0.0000	0.0000	0.1008	0.0523	0.2433	0.1213	0.1261	0.0000
Q9H444	128866	CHMP4B	0.0000	0.0000	0.1008	0.1308	0.0000	0.0000	0.0000	0.0000
Q9NPA0	56851	EMC7	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NRW1	51560	RAB6B	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q9NV66	55253	TYW1	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NW15	55129	ANO10	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NWV4	54987	C1orf123	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.0000	0.0000
Q9UH65	23075	SWAP70	0.0000	0.0000	0.1008	0.0785	0.1622	0.1213	0.1892	0.0000
Q9UKV5	267	AMFR	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q9UL46	5721	PSME2	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.0000	0.0000
Q9Y478	5564	PRKAB1	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.0000	0.0000
Q9Y5V3	9500	MAGED1	0.0000	0.0000	0.1008	0.0785	0.0000	0.1213	0.1892	0.0000
Q9Y6M7-3	9497	SLC4A7	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.0000	0.0000
Q9Y6X4	26049	FAM169A	0.0000	0.0000	0.1008	0.2093	0.0000	0.0000	0.0000	0.0000
Q9UBF2	26958	COPG2	0.0000	0.0000	0.9073	0.4186	0.0000	0.1213	0.3783	0.3081
O75410	6867	TACC1	0.0000	0.0000	0.7056	0.4971	0.3244	0.3639	0.1261	0.1232
Q8NC51	26135	SERBP1	0.0000	0.0000	0.5040	0.3663	0.4866	0.4245	1.1349	0.9242
P16949	3925	STMN1	0.0000	0.0000	0.4536	0.3401	0.1622	0.1213	1.5763	1.2939
Q96MW1	124808	CCDC43	0.0000	0.0000	0.4536	0.4186	0.1622	0.1213	0.4414	0.4929

P0DMV8	3303	HSPA1A	0.0000	0.0000	0.4032	0.3140	0.6488	0.6064	0.7566	0.4313
Q15942	7791	ZYX	0.0000	0.0000	0.4032	0.2093	0.0000	0.0000	0.4414	0.6778
P21333	2316	FLNA	0.0000	0.0000	0.3528	0.2616	0.7299	0.7277	2.2068	2.0949
P50990	10694	CCT8	0.0000	0.0000	0.3528	0.2616	0.4055	0.5458	1.5763	1.1707
P29590	5371	PML	0.0000	0.0000	0.3024	0.1047	0.0000	0.1213	0.2522	0.3081
Q15555	10982	MAPRE2	0.0000	0.0000	0.3024	0.1832	0.4055	0.4245	0.4414	0.4929
Q15691	22919	MAPRE1	0.0000	0.0000	0.3024	0.1832	0.0000	0.0000	0.1892	0.3081
Q9UJU6	28988	DBNL	0.0000	0.0000	0.2520	0.3401	0.0000	0.0000	0.5675	0.4313
Q9UQN3	25978	CHMP2B	0.0000	0.0000	0.2520	0.3401	0.1622	0.1213	0.5675	0.4313
O14737	9141	PDCD5	0.0000	0.0000	0.2016	0.2093	0.3244	0.3032	0.3783	0.1848
P13639	1938	EEF2	0.0000	0.0000	0.2016	0.1047	0.0000	0.3639	0.3153	0.2465
Q13765	4666	NACA	0.0000	0.0000	0.2016	0.1308	0.0000	0.0000	0.1261	0.2465
Q8TF01	25957	PNISR	0.0000	0.0000	0.2016	0.0785	0.1622	0.1213	0.1261	0.1232
Q96C19	79180	EFHD2	0.0000	0.0000	0.2016	0.1047	0.2433	0.1819	0.2522	0.1848
O14654	8471	IRS4	0.0000	0.0000	0.1512	0.1308	0.2433	0.0000	0.3153	0.4313
O43639	8440	NCK2	0.0000	0.0000	0.1512	0.0523	0.0000	0.1819	0.2522	0.1848
P08670	7431	VIM	0.0000	0.0000	0.1512	0.1308	0.0000	0.1213	0.7566	0.6161
P13797	5358	PLS3	0.0000	0.0000	0.1512	0.0785	0.0000	0.1213	0.1892	0.1232
P16333	4690	NCK1	0.0000	0.0000	0.1512	0.0523	0.0000	0.1819	0.2522	0.1848
P23588	1975	EIF4B	0.0000	0.0000	0.1512	0.1832	0.0000	0.0000	0.3153	0.4929
P27816	4134	MAP4	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.6936	1.3555
P55196	4301	MLLT4	0.0000	0.0000	0.1512	0.0785	0.0000	0.1213	0.3783	0.3081
P68104	1915	EEF1A1	0.0000	0.0000	0.1512	0.2093	0.9732	0.6671	0.5675	0.4929
Q14980	4926	NUMA1	0.0000	0.0000	0.1512	0.0523	0.1622	0.3639	0.3153	0.2465
Q15545	6879	TAF7	0.0000	0.0000	0.1512	0.1047	0.3244	0.2426	0.3153	0.2465
Q96EB1	26610	ELP4	0.0000	0.0000	0.1512	0.1047	0.0000	0.1213	0.1892	0.2465
Q9H3U1	55898	UNC45A	0.0000	0.0000	0.1512	0.0785	0.1622	0.1819	0.3783	0.1232
Q9NR12	9260	PDLIM7	0.0000	0.0000	0.1512	0.0523	0.1622	0.1213	0.1261	0.1848
Q9UKX7	10762	NUP50	0.0000	0.0000	0.1512	0.1570	0.0000	0.0000	0.1892	0.1848
A6NKD9	317762	CCDC85C	0.0000	0.0000	0.1008	0.0785	0.4866	0.3032	0.4414	0.3081
O14531	10570	DPYSL4	0.0000	0.0000	0.1008	0.0523	0.1622	0.0000	0.3153	0.1848
O75534	7812	CSDE1	0.0000	0.0000	0.1008	0.1570	0.0000	0.0000	0.5675	0.4929
O76041	10529	NEBL	0.0000	0.0000	0.1008	0.0785	0.1622	0.1213	0.2522	0.1232
O94842	9878	TOX4	0.0000	0.0000	0.1008	0.1308	0.4866	0.2426	0.4414	0.4929
P13861	5576	PRKAR2A	0.0000	0.0000	0.1008	0.0523	0.6488	0.7884	0.2522	0.1848
P20290	689	BTF3	0.0000	0.0000	0.1008	0.1832	0.0000	0.0000	0.1261	0.1848
P25685	3337	DNAJB1	0.0000	0.0000	0.1008	0.0523	0.1622	0.1819	0.2522	0.2465
P30419	4836	NMT1	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.1892	0.2465
P30876	5431	POLR2B	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.1261	0.1232
P31948	10963	STIP1	0.0000	0.0000	0.1008	0.1308	0.0000	0.0000	0.2522	0.3081

P42224	6772	STAT1	0.0000	0.0000	0.1008	0.0523	0.0000	0.2426	0.3153	0.2465
P43487	5902	RANBP1	0.0000	0.0000	0.1008	0.1308	0.2433	0.2426	0.2522	0.4929
P46821	4131	MAP1B	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.3153	0.2465
P48444	372	ARCN1	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.2522	0.1848
P54577	8565	YARS	0.0000	0.0000	0.1008	0.0000	0.0000	0.0000	0.3153	0.2465
P61247	6189	RPS3A	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.2522	0.2465
Q13596	6642	SNX1	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.2522	0.3081
Q14008	9793	CKAP5	0.0000	0.0000	0.1008	0.1047	0.4866	0.6064	0.5675	0.3697
Q15036	9784	SNX17	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.1261	0.1232
Q15121	8682	PEA15	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.1261	0.1232
Q15233	4841	NONO	0.0000	0.0000	0.1008	0.1308	0.0000	0.1213	0.5675	0.3697
Q5VZ89	55667	DENND4C	0.0000	0.0000	0.1008	0.0785	0.1622	0.1213	0.1892	0.1232
Q71U36	7846	TUBA1A	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.2522	0.1848
Q8IXW5	79871	RPAP2	0.0000	0.0000	0.1008	0.0785	0.1622	0.2426	0.1892	0.1848
Q8WW12	57092	PCNP	0.0000	0.0000	0.1008	0.1570	0.2433	0.0000	0.5044	0.6161
Q96BY7	55102	ATG2B	0.0000	0.0000	0.1008	0.0523	0.0000	0.1819	0.1261	0.1232
Q96CT7	115098	CCDC124	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.1261	0.1232
Q96EB1-3	26610	ELP4	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.1261	0.1232
Q96HC4	10611	PDLIM5	0.0000	0.0000	0.1008	0.0785	0.1622	0.1213	0.3783	0.2465
Q99567	4927	NUP88	0.0000	0.0000	0.1008	0.0523	0.0000	0.1213	0.1261	0.1232
Q9H5V9	63932	CXorf56	0.0000	0.0000	0.1008	0.1832	0.4055	0.4245	0.4414	0.4313
Q9NPI6	55802	DCP1A	0.0000	0.0000	0.1008	0.1832	0.1622	0.3032	0.3153	0.3697
Q9NT62	64422	ATG3	0.0000	0.0000	0.1008	0.0785	0.0000	0.0000	0.1892	0.1232
Q9UQR0	10389	SCML2	0.0000	0.0000	0.1008	0.0523	0.1622	0.1213	0.2522	0.2465
Q9Y2S6	51372	TMA7	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.1261	0.1232
Q9Y490	7094	TLN1	0.0000	0.0000	0.1008	0.1047	0.0000	0.0000	0.3153	0.2465
Q9Y4K4	11183	MAP4K5	0.0000	0.0000	0.1008	0.0523	0.0000	0.0000	0.1261	0.1232
Q9UNL2	6747	SSR3	0.0000	0.0000	0.0000	0.2616	0.0000	0.0000	0.0000	0.0000
Q5JSH3	54521	WDR44	0.0000	0.0000	0.0000	0.2355	0.0000	0.0000	0.0000	0.0000
O00151	9124	PDLIM1	0.0000	0.0000	0.0000	0.2093	0.0000	0.0000	0.2522	0.0000
Q9C037	89122	TRIM4	0.0000	0.0000	0.0000	0.2093	0.0000	0.3639	0.0000	0.0000
Q9H1P3	9885	OSBPL2	0.0000	0.0000	0.0000	0.2093	0.0000	0.0000	0.0000	0.0000
Q9HC62	59343	SENP2	0.0000	0.0000	0.0000	0.2093	0.0000	0.0000	0.0000	0.0000
Q04323	51035	UBXN1	0.0000	0.0000	0.0000	0.1832	0.0000	0.0000	0.0000	0.0000
Q15042	22930	RAB3GAP1	0.0000	0.0000	0.0000	0.1832	0.0000	0.0000	0.0000	0.0000
Q9C0C9	63893	UBE2O	0.0000	0.0000	0.0000	0.1570	0.0000	0.0000	0.1892	0.0000
Q9NXW2	54788	DNAJB12	0.0000	0.0000	0.0000	0.1570	0.0000	0.0000	0.0000	0.0000
O15269	10558	SPTLC1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
P31689	3301	DNAJA1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
P61923	22818	COPZ1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.1892	0.0000

Q14BN4	7871	SLMAP	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q6NXT6	202018	TAPT1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q7KZF4	27044	SND1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.1232
Q86W74	157567	ANKRD46	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q8WXH0	23224	SYNE2	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q9BVW5	54962	TIPIN	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q9H446	51389	RWDD1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q9P0U3	29843	SENP1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q9P246	57620	STIM2	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q9UJ14	2686	GGT7	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q9ULH0	57498	KIDINS220	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
Q9Y678	22820	COPG1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.0000	0.0000
O00213	322	APBB1	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
O14966	8934	RAB29	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
O43402	10328	EMC8	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
O60499	8677	STX10	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
O75794	8872	CDC123	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
O95573	2181	ACSL3	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
P49914	10588	MTHFS	0.0000	0.0000	0.0000	0.1047	0.0000	0.1819	0.0000	0.0000
P53618	1315	COPB1	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
P60709	60	ACTB	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
P62987	7311	UBA52	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
Q15025	10318	TNIP1	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
Q3ZAQ7	203547	VMA21	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
Q53T59	64342	HS1BP3	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
Q9BXB4	114885	OSBPL11	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
Q9H902	65055	REEP1	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
Q9Y265	8607	RUVBL1	0.0000	0.0000	0.0000	0.1047	0.2433	0.1213	0.2522	0.0000
Q9Y295	4733	DRG1	0.0000	0.0000	0.0000	0.1047	0.1622	0.1213	0.0000	0.1232
Q9Y2K6	10868	USP20	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.0000	0.0000
B7ZAQ6	51463	GPR89A	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O00232	5718	PSMD12	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O00559	9166	EBAG9	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O00750	5287	PIK3C2B	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O14562	56061	UBFD1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O14653	9570	GOSR2	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O43719	27336	HTATSF1	0.0000	0.0000	0.0000	0.0785	0.1622	0.1213	0.0000	0.0000
O43752	10228	STX6	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O94898	9860	LRIG2	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
O95197	10313	RTN3	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000

O96005	1209	CLPTM1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P08195	6520	SLC3A2	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P11717	3482	IGF2R	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P13498	1535	CYBA	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P16615	488	ATP2A2	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P18085	378	ARF4	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P22234	10606	PAICS	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.2465
P24522	1647	GADD45A	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P38606	523	ATP6V1A	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P49773	3094	HINT1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.1848
P51149	7879	RAB7A	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P54252	4287	ATXN3	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P56211	10776	ARPP19	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.2522	0.0000
P57737-3	79585	CORO7	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P63313	9168	TMSB10	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P67870	1460	CSNK2B	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
P78381-2	7355	SLC35A2	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q05655	5580	PRKCD	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q12792	5756	TWF1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q12893	11070	TMEM115	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q13308	5754	PTK7	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q13370	5140	PDE3B	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q6IAA8	55004	LAMTOR1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q6PKG0	23367	LARP1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q6ZNB6	152518	NFXL1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q70UQ0	121457	IKBIP	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q86UL3	137964	AGPAT6	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q8TAT6	55666	NPLOC4	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q8WYP5	25909	AHCTF1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q96JB5	80279	CDK5RAP3	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q96LB3	80173	IFT74	0.0000	0.0000	0.0000	0.0785	0.2433	0.1213	0.0000	0.0000
Q96LT7	203228	C9orf72	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q9BVT8	83590	TMUB1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q9H0A8	54939	COMMD4	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q9NU53	116254	GINM1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q9NVR5	55172	DNAAF2	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.1892	0.0000
Q9UBS9	51430	SUCO	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q9UI30	51504	TRMT112	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000
Q9Y508	55905	RNF114	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.1232
Q9Y6B6	51128	SAR1B	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.0000	0.0000

O00154	11332	ACOT7	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O00560	6386	SDCBP	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O14523	9854	C2CD2L	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O14530	10190	TXNDC9	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1892	0.0000
O14656	1861	TOR1A	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O15131	3841	KPNA5	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O15357	3636	INPPL1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.0000
O60566	701	BUB1B	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O75190-2	10049	DNAJB6	0.0000	0.0000	0.0000	0.0523	0.1622	0.0000	0.0000	0.1232
O75976	1362	CPD	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O76024	7466	WFS1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O76080	7763	ZFAND5	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1848
O94830	23259	DDHD2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O94901	23353	SUN1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O94991	26050	SLITRK5	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O95067	9133	CCNB2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
O95684	11116	FGFR1OP	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.0000	0.1232
O95816	9532	BAG2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P02545	4000	LMNA	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P08243	440	ASNS	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P09234	6631	SNRPC	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P09496	1211	CLTA	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1848
P11441	8266	UBL4A	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P12270	7175	TPR	0.0000	0.0000	0.0000	0.0523	0.1622	0.0000	0.0000	0.0000
P12277	1152	CKB	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P13693	7178	TPT1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P15170-2	2935	GSPT1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P15260	3459	IFNGR1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P15531	4830	NME1	0.0000	0.0000	0.0000	0.0523	0.1622	0.3032	0.0000	0.0000
P20020	490	ATP2B1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P25789	5685	PSMA4	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P30086	5037	PEBP1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P31350	6241	RRM2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P31939	471	ATIC	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P31946	7529	YWHAB	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.0000
P35606	9276	COPB2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P35613	682	BSG	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P40394	131	ADH7	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P42702	3977	LIFR	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P48634	7916	PRRC2A	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.2522	0.0000

P49588	16	AARS	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P49753	10965	ACOT2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P49768	5663	PSEN1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P50542	5830	PEX5	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P50914	9045	RPL14	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P51809	6845	VAMP7	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P55209	4673	NAP1L1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P60866	6224	RPS20	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1232
P61011	6729	SRP54	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P62826	5901	RAN	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P78310	1525	CXADR	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
P98170	331	XIAP	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q01968	4952	OCRL	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q0GE19	84068	SLC10A7	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q13283	10146	G3BP1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1848
Q13330	9112	MTA1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q13347	8668	EIF3I	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q13563	5311	PKD2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q13705	93	ACVR2B	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q13948	1523	CUX1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q14320	9130	FAM50A	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1892	0.0000
Q15126	10654	PMVK	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q15154	5108	PCM1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q15813	6905	TBCE	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q16526	1407	CRY1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q16527	1466	CSRP2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q4VCS5	154796	AMOT	0.0000	0.0000	0.0000	0.0523	1.3788	1.5767	0.1892	0.0000
Q53GS7	2733	GLE1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q5T8D3	91452	ACBD5	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q68DQ2	131544	CRYBG3	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q6I9Y2	80145	THOC7	0.0000	0.0000	0.0000	0.0523	0.2433	0.0000	0.0000	0.0000
Q6NW29	201965	RWDD4	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q6NXS1	0	PPP1R2P3	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1232
Q6P1R3	79684	MSANTD2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q6P2H8	79639	TMEM53	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q6P499	57185	NIPAL3	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q6ZUT1	55216	C11orf57	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.1261	0.0000
Q71RG4	79089	TMUB2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8IVD9	23386	NUDCD3	0.0000	0.0000	0.0000	0.0523	0.0000	0.1213	0.0000	0.1232
Q8IW50	203259	FAM219A	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000

Q8IWC1	79649	MAP7D3	0.0000	0.0000	0.0000	0.0523	0.0000	0.2426	0.0000	0.1232
Q8IX94	1E+08	CTAGE4	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8IZE3	57147	SCYL3	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8IZJ1	219699	UNC5B	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8N0X7	23111	SPG20	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8N5I9	121053	C12orf45	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.0000	0.0000
Q8N6L1	200185	KRTCAP2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8NCS4	1.01E+08	ZMYM6NB	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8NFH3	348995	NUP43	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q8NFH5	129401	NUP35	0.0000	0.0000	0.0000	0.0523	0.2433	0.1213	0.0000	0.0000
Q8NHP6	158747	MOSPD2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q92504	7922	SLC39A7	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q92545	23505	TMEM131	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q92551	9807	IP6K1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q92953	9312	KCNB2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q96D71	85021	REPS1	0.0000	0.0000	0.0000	0.0523	0.1622	0.1819	0.1892	0.0000
Q96E22	116150	NUS1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q96FZ7	79643	CHMP6	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q96J01	84321	THOC3	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q96KN1	157638	FAM84B	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q96N66	79143	MBOAT7	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q99442	7095	SEC62	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q99590	9169	SCAF11	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q99675	10668	CGRRF1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q99808	2030	SLC29A1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9BQA1	79084	WDR77	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.0000
Q9BQE4	55829	VIMP	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9BSW2	84766	CRACR2A	0.0000	0.0000	0.0000	0.0523	0.0000	0.1213	0.0000	0.0000
Q9BV40	8673	VAMP8	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9BVM2	25911	DPCD	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9H098	83641	FAM107B	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1848
Q9H267	26276	VPS33B	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9H2J7	55117	SLC6A15	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9H6H4	80346	REEP4	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9H8Y8	26003	GORASP2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9HD20	57130	ATP13A1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NP72	22931	RAB18	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NP73-2	79868	ALG13	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NPJ6	29079	MED4	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NQ48	54585	LZTFL1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.3081

Q9NQG6	54471	MIEF1	0.0000	0.0000	0.0000	0.0523	0.0000	0.1213	0.0000	0.0000
Q9NR31	56681	SAR1A	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NRN7	60496	AASDHPPT	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NTN3	23169	SLC35D1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9NX08	54951	COMMD8	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1232
Q9NX40-4	54940	OCIAD1	0.0000	0.0000	0.0000	0.0523	0.3244	0.1213	0.0000	0.0000
Q9NZ01	9524	TECR	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9P0K7	26064	RAI14	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.1848
Q9UGI8	26136	TES	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9UI14	10567	RABAC1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9UL25	23011	RAB21	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9ULE6	27143	PALD1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9ULU4	23613	ZMYND8	0.0000	0.0000	0.0000	0.0523	0.0000	0.1213	0.0000	0.0000
Q9Y4R8	9894	TELO2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q9Y5P4	10087	COL4A3BP	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.0000	0.0000
Q15417	1266	CNN3	0.0000	0.0000	0.0000	0.2878	0.0000	0.1819	0.5044	0.5545
Q04637	1981	EIF4G1	0.0000	0.0000	0.0000	0.2616	0.1622	0.3032	1.4502	1.3555
O00571	1654	DDX3X	0.0000	0.0000	0.0000	0.2355	0.0000	0.0000	0.2522	0.3081
P49959	4361	MRE11A	0.0000	0.0000	0.0000	0.2093	0.4866	0.6064	0.3783	0.4929
Q9UKY7	55573	CDV3	0.0000	0.0000	0.0000	0.2093	0.1622	0.1213	0.5675	0.6161
O00193	10944	SMAP	0.0000	0.0000	0.0000	0.1832	0.3244	0.3032	0.4414	0.4313
P13984	2963	GTF2F2	0.0000	0.0000	0.0000	0.1308	0.3244	0.2426	0.2522	0.3081
P52594	3267	AGFG1	0.0000	0.0000	0.0000	0.1308	0.3244	0.3032	0.1261	0.1848
Q05682	800	CALD1	0.0000	0.0000	0.0000	0.1308	0.2433	0.3639	0.5675	0.3081
Q6IBS0	11344	TWF2	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.1892	0.1848
Q99961	6455	SH3GL1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.1892	0.1848
Q9NSA3	56998	CTNNBIP1	0.0000	0.0000	0.0000	0.1308	0.0000	0.0000	0.1892	0.1848
O75886	10254	STAM2	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.3783	0.2465
O95218	9406	ZRANB2	0.0000	0.0000	0.0000	0.1047	0.0000	0.1819	0.3153	0.4313
P49792	5903	RANBP2	0.0000	0.0000	0.0000	0.1047	0.0000	0.0000	0.7566	0.3081
Q15365	5093	PCBP1	0.0000	0.0000	0.0000	0.1047	0.4866	0.3639	0.5044	0.3081
Q7Z569	8315	BRAP	0.0000	0.0000	0.0000	0.1047	0.0000	0.1213	0.3153	0.2465
Q8N6N3	148423	C1orf52	0.0000	0.0000	0.0000	0.1047	0.1622	0.0000	0.3783	0.1232
Q9P013	51503	CWC15	0.0000	0.0000	0.0000	0.1047	0.3244	0.1819	0.3153	0.3697
Q9Y266	10726	NUDC	0.0000	0.0000	0.0000	0.1047	0.1622	0.1213	0.5675	0.4313
O15084	23243	ANKRD28	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.1261	0.2465
O60869	8721	EDF1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.1892	0.1848
O75179	26057	ANKRD17	0.0000	0.0000	0.0000	0.0785	0.1622	0.1819	0.2522	0.3081
O75937	22826	DNAJC8	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.3783	0.2465
P06748	4869	NPM1	0.0000	0.0000	0.0000	0.0785	2.9197	2.3044	0.9458	0.8626

P37840	6622	SNCA	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.1261	0.1848
Q13442	11333	PDAP1	0.0000	0.0000	0.0000	0.0785	0.3244	0.1819	0.2522	0.3081
Q15652	221037	JMJD1C	0.0000	0.0000	0.0000	0.0785	0.1622	0.1213	0.1892	0.1848
Q6FI81	57019	CIAPIN1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.1261	0.1848
Q7Z4V5	84717	HDGFRP2	0.0000	0.0000	0.0000	0.0785	0.2433	0.1213	0.1892	0.1232
Q96JH7	80124	VCPIP1	0.0000	0.0000	0.0000	0.0785	0.3244	0.2426	0.3783	0.3697
Q9HB71	27101	CACYBP	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.1892	0.2465
Q9UK76	51155	HN1	0.0000	0.0000	0.0000	0.0785	0.0000	0.0000	0.2522	0.2465
Q9Y520	23215	PRRC2C	0.0000	0.0000	0.0000	0.0785	0.1622	0.1213	0.5044	0.7394
O00418	1.02E+08	EEF2K	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1232
O43399	7165	TPD52L2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1232
O95817	9531	BAG3	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.1261	0.1232
P06737	5836	PYGL	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1232
P09661	6627	SNRPA1	0.0000	0.0000	0.0000	0.0523	0.2433	0.1213	0.5044	0.4929
P19338	4691	NCL	0.0000	0.0000	0.0000	0.0523	1.0543	0.5458	0.7566	0.8010
P24534	1933	EEF1B2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1232
P33240	1478	CSTF2	0.0000	0.0000	0.0000	0.0523	0.1622	0.2426	0.3153	0.2465
P50851	987	LRBA	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1892	0.1232
P51991	220988	HNRNPA3	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.2522	0.1232
P52732	3832	KIF11	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.2522	0.3081
Q13435	10992	SF3B2	0.0000	0.0000	0.0000	0.0523	0.4866	0.4851	0.5044	0.3697
Q147X3	122830	NAA30	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1848
Q15003	23397	NCAPH	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1848
Q3MHD2	124801	LSM12	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1232
Q5T8P6	64062	RBM26	0.0000	0.0000	0.0000	0.0523	0.2433	0.3032	0.3153	0.1848
Q6EEV4-2	81488	POLR2M	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.1261	0.1232
Q6XZF7	23268	DNMBP	0.0000	0.0000	0.0000	0.0523	0.0000	0.1213	0.1261	0.1232
Q7L014	9879	DDX46	0.0000	0.0000	0.0000	0.0523	0.4866	0.3639	0.9458	0.7394
Q8IWJ2	9648	GCC2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.2522	0.1232
Q8N7H5	54623	PAF1	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.1892	0.1232
Q8NBF2	374354	NHLRC2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1232
Q8TEQ6	25929	GEMIN5	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.3783	0.1848
Q93045	11075	STMN2	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.3783	0.2465
Q96PZ0	54517	PUS7	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.1261	0.1232
Q9GZT9	54583	EGLN1	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1261	0.1232
Q9H0L4	23283	CSTF2T	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.1261	0.1232
Q9H467	79004	CUEDC2	0.0000	0.0000	0.0000	0.0523	0.2433	0.1213	0.1892	0.1232
Q9NRA8	56478	EIF4ENIF1	0.0000	0.0000	0.0000	0.0523	2.0276	1.6374	0.1261	0.1848
Q9NYF8	9774	BCLAF1	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	1.0088	0.7394
Q9UHR5	29115	SAP30BP	0.0000	0.0000	0.0000	0.0523	0.3244	0.3032	0.3153	0.2465

Q9UKK9	11164	NUDT5	0.0000	0.0000	0.0000	0.0523	0.0000	0.0000	0.1892	0.1848
Q9Y450-2	10767	HBS1L	0.0000	0.0000	0.0000	0.0523	0.1622	0.1213	0.1261	0.1232
O00429	10059	DNM1L	0.0000	0.0000	0.0000	0.0000	1.6221	1.2129	0.0000	0.0000
P06748-3	4869	NPM1	0.0000	0.0000	0.0000	0.0000	0.4866	0.1819	0.0000	0.0000
P33981	7272	TTK	0.0000	0.0000	0.0000	0.0000	0.4866	0.3032	0.0000	0.0000
P40855	5824	PEX19	0.0000	0.0000	0.0000	0.0000	0.4866	0.3032	0.0000	0.0000
Q9H792	79834	PEAK1	0.0000	0.0000	0.0000	0.0000	0.4866	0.4851	0.0000	0.0000
O00429-4	10059	DNM1L	0.0000	0.0000	0.0000	0.0000	0.3244	0.2426	0.0000	0.0000
P06730	1977	EIF4E	0.0000	0.0000	0.0000	0.0000	0.3244	0.1819	0.1892	0.0000
P11586	4522	MTHFD1	0.0000	0.0000	0.0000	0.0000	0.3244	0.5458	0.0000	0.0000
Q12983	664	BNIP3	0.0000	0.0000	0.0000	0.0000	0.3244	0.1213	0.0000	0.0000
Q13573	22938	SNW1	0.0000	0.0000	0.0000	0.0000	0.3244	0.3032	0.0000	0.0000
Q5VT52	23248	RPRD2	0.0000	0.0000	0.0000	0.0000	0.3244	0.4851	0.1261	0.0000
Q86VM9	124245	ZC3H18	0.0000	0.0000	0.0000	0.0000	0.3244	0.0000	0.0000	0.0000
Q9HCH0	57701	NCKAP5L	0.0000	0.0000	0.0000	0.0000	0.3244	0.3032	0.0000	0.0000
O60238	665	BNIP3L	0.0000	0.0000	0.0000	0.0000	0.2433	0.2426	0.0000	0.0000
P51970	4702	NDUFA8	0.0000	0.0000	0.0000	0.0000	0.2433	0.1213	0.0000	0.0000
Q6Y7W6	26058	GIGYF2	0.0000	0.0000	0.0000	0.0000	0.2433	0.0000	0.0000	0.2465
Q9NPA3	58526	MID1IP1	0.0000	0.0000	0.0000	0.0000	0.2433	0.2426	0.0000	0.0000
Q9UPQ9	23112	TNRC6B	0.0000	0.0000	0.0000	0.0000	0.2433	0.2426	0.0000	0.0000
O00429-2	10059	DNM1L	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
O00429-3	10059	DNM1L	0.0000	0.0000	0.0000	0.0000	0.1622	0.1819	0.0000	0.0000
O14976	2580	GAK	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
O75683	6838	SURF6	0.0000	0.0000	0.0000	0.0000	0.1622	0.1819	0.0000	0.0000
O95202	3954	LETM1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
O96011	8799	PEX11B	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
P10809	3329	HSPD1	0.0000	0.0000	0.0000	0.0000	0.1622	0.3032	0.0000	0.0000
P19532	7030	TFE3	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.1848
P28347	7003	TEAD1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
P40939	3030	HADHA	0.0000	0.0000	0.0000	0.0000	0.1622	0.1819	0.0000	0.0000
P43243	9782	MATR3	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
P52758	10247	HRSP12	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q12815	10024	TROAP	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q14687	23199	GSE1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.1261	0.0000
Q14978	9221	NOLC1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1819	0.0000	0.1848
Q15390	9650	MTFR1	0.0000	0.0000	0.0000	0.0000	0.1622	0.4245	0.0000	0.0000
Q5SZL2	387119	CEP85L	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q5UIP0	55183	RIF1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.1848
Q6P444	113115	MTFR2	0.0000	0.0000	0.0000	0.0000	0.1622	0.1819	0.0000	0.0000
Q7L0Y3	54931	TRMT10C	0.0000	0.0000	0.0000	0.0000	0.1622	0.1819	0.0000	0.0000

Q7L5Y9	10296	MAEA	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q86UW6	55728	N4BP2	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.1232
Q8N9T8	65095	KRI1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q8TCU4	7840	ALMS1	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q8TDF5	81832	NETO1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q96IK1	91272	BOD1	0.0000	0.0000	0.0000	0.0000	0.1622	0.2426	0.0000	0.0000
Q96RE7	112939	NACC1	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.1261	0.0000
Q99856	1820	ARID3A	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q9BRK4	84445	LZTS2	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q9BW92	80222	TARS2	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q9BY89	85379	KIAA1671	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q9BZD4	83540	NUF2	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q9H019	56181	MTFR1L	0.0000	0.0000	0.0000	0.0000	0.1622	0.2426	0.0000	0.0000
Q9H3R0	23081	KDM4C	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q9H871	64795	RMND5A	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q9NPL8	51300	TIMMDC1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.0000	0.0000
Q9NSI2	85395	FAM207A	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q9NSV4	81624	DIAPH3	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q9NVU7	55153	SDAD1	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.1232
Q9UKJ3	23131	GPATCH8	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.0000	0.0000
Q13428	6949	TCOF1	0.0000	0.0000	0.0000	0.0000	0.8110	0.7884	0.5675	0.6161
O75381	5195	PEX14	0.0000	0.0000	0.0000	0.0000	0.4866	0.4245	0.1261	0.3697
Q5VUA4	24149	ZNF318	0.0000	0.0000	0.0000	0.0000	0.4866	0.1819	0.1892	0.1232
Q96DF8	8220	DGCR14	0.0000	0.0000	0.0000	0.0000	0.4866	0.4245	0.3153	0.3081
O75533	23451	SF3B1	0.0000	0.0000	0.0000	0.0000	0.4055	0.3639	0.5044	0.4313
P51610	3054	HCFC1	0.0000	0.0000	0.0000	0.0000	0.3244	0.4245	0.6936	0.8010
Q9H501	51575	ESF1	0.0000	0.0000	0.0000	0.0000	0.3244	0.3032	0.2522	0.2465
Q9Y2Z0	10910	SUGT1	0.0000	0.0000	0.0000	0.0000	0.3244	0.2426	0.3153	0.1848
O75528	10474	TADA3	0.0000	0.0000	0.0000	0.0000	0.2433	0.3639	0.1261	0.2465
O95391	10569	SLU7	0.0000	0.0000	0.0000	0.0000	0.2433	0.1819	0.1261	0.1232
P52597	3185	HNRNPF	0.0000	0.0000	0.0000	0.0000	0.2433	0.2426	0.1892	0.1232
Q6W2J9	54880	BCOR	0.0000	0.0000	0.0000	0.0000	0.2433	0.1213	0.1261	0.1232
P53999	10923	SUB1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.1261	0.1232
P55081	4236	MFAP1	0.0000	0.0000	0.0000	0.0000	0.1622	0.1819	0.2522	0.1848
Q13148	23435	TARDBP	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.1261	0.1848
Q8IVW6	10620	ARID3B	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.3153	0.2465
Q96KR1	51663	ZFR	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.1261	0.1232
Q96N46	151613	TTC14	0.0000	0.0000	0.0000	0.0000	0.1622	0.1213	0.1261	0.1232
Q9UIF9	11176	BAZ2A	0.0000	0.0000	0.0000	0.0000	0.1622	0.0000	0.3153	0.1848
P35658	8021	NUP214	0.0000	0.0000	0.0000	0.0000	0.0000	0.3032	0.0000	0.0000

P38646	3313	HSPA9	0.0000	0.0000	0.0000	0.0000	0.0000	0.2426	0.0000	0.0000
P52272	4670	HNRNPM	0.0000	0.0000	0.0000	0.0000	0.0000	0.2426	0.0000	0.1848
Q08211	1660	DHX9	0.0000	0.0000	0.0000	0.0000	0.0000	0.2426	0.1892	0.0000
Q8IWZ3	404734	ANKHD1	0.0000	0.0000	0.0000	0.0000	0.0000	0.2426	0.0000	0.0000
P00338	3939	LDHA	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
P05141	292	SLC25A5	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
Q76FK4	55035	NOL8	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
Q8IX90	221150	SKA3	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
Q8IY67-2	125950	RAVER1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
Q8N2A8	201164	PLD6	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
Q96LZ7	151393	RMDN2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
Q96PU8	9444	QKI	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.0000	0.0000
O14979	9987	HNRNPDL	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.1232
O15355	5496	PPM1G	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P09972	230	ALDOC	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P15822	3096	HIVEP1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P15880	6187	RPS2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1261	0.0000
P19367	3098	HK1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P35637	2521	FUS	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.1848
P38432	8161	COIL	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P42694	0	HELZ	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P51587	675	BRCA2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P56962	55014	STX17	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q16740	8192	CLPP	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q5JSZ5	84726	PRRC2B	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1261	0.0000
Q5QJE6	30836	DNTTIP2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q5TC12	64756	ATPAF1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q6P2H3	64793	CEP85	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q6ZRV2	286077	FAM83H	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q7Z2W4-4	56829	ZC3HAV1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q7Z5K2	23063	WAPAL	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1892	0.0000
Q86T24	10009	ZBTB33	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q86XN7	80209	PROSER1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q8IV38	57037	ANKMY2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q8IWB9	55852	TEX2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.1232
Q8N1G0	57592	ZNF687	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q8NI36	134430	WDR36	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q8WU79	64744	SMAP2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q92922	6599	SMARCC1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q96AY4	23331	TTC28	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000

Q96EV2	155435	RBM33	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q9BQ52	60528	ELAC2	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q9BRQ6	84303	CHCHD6	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q9BTC0	11083	DIDO1	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1261	0.0000
Q9BY77	84271	POLDIP3	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q9BYC9	55052	MRPL20	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
Q9Y5Y5	9409	PEX16	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.0000	0.0000
P07195	3945	LDHB	0.0000	0.0000	0.0000	0.0000	0.0000	0.2426	0.1261	0.1232
Q00839	3192	HNRNPU	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.1892	0.3081
Q13123	3550	IK	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.1261	0.3081
Q16630	11052	CPSF6	0.0000	0.0000	0.0000	0.0000	0.0000	0.1819	0.2522	0.2465
Q05519	9295	SRSF11	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1892	0.1848
Q15020	9733	SART3	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1892	0.3081
Q6PII3	51244	CCDC174	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1261	0.1232
Q99426	1155	TBCB	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1892	0.1848
Q9H2P0	23394	ADNP	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1892	0.1848
Q9H814	51808	PHAX	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.2522	0.1848
Q9Y520-7	23215	PRRC2C	0.0000	0.0000	0.0000	0.0000	0.0000	0.1213	0.1261	0.1232
O15083	26059	ERC2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
O43432	8672	EIF4G3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1848
O43491	2037	EPB41L2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.5675	0.5545
O60716	1500	CTNND1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1848
O60749	6643	SNX2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3783	0.3081
O75312	8882	ZPR1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.0000
O75821	8666	EIF3G	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3153	0.1232
O75874	3417	IDH1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1848
P05388	6175	RPLP0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.0000
P06753	7170	TPM3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
P07814	2058	EPRS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3153	0.2465
P10636-2	4137	MAPT	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1848
P11171	2035	EPB41	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.2465
P14866	3191	HNRNPL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
P15924	1832	DSP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3783	0.3697
P18583	6651	SON	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.0000
P23381	7453	WARS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
P27694	6117	RPA1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3783	0.3081
P29692	1936	EEF1D	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1232
P35579	4627	MYH9	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3153	0.2465
P40227	908	CCT6A	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1848
P49454	1063	CENPF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000

P49643	5558	PRIM2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
P49750	56252	YLPM1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3153	0.4313
P51858	3068	HDGF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
P53367	27236	ARFIP1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
P78371	10576	CCT2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.0000
P85037	221937	FOXK1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q00341	3069	HDLBP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.6305	0.5545
Q01780	5394	EXOSC10	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1848
Q04724	7088	TLE1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1848
Q04726	7090	TLE3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q07157	7082	TJP1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3783	0.3081
Q09666	79026	AHNAK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.6936	0.9242
Q12955-4	288	ANK3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q12959	1739	DLG1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q13129	6018	RLF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q13206	1662	DDX10	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.2465
Q13561	10540	DCTN2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q14839	1108	CHD4	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3783	0.3081
Q15424	6294	SAFB	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.2465
Q15459	10291	SF3A1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3153	0.3697
Q16594	6880	TAF9	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q2TAL8	54870	QRICH1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q2VIR3	0	EIF2S3L	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q5SW79	9859	CEP170	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3153	0.3697
Q5T5U3	57584	ARHGAP21	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1848
Q5VWQ0	54665	RSBN1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q6IN85	55671	SMEK1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1848
Q6NSI4	55086	CXorf57	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1232
Q6P2Q9	10594	PRPF8	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.0000
Q6UN15	81608	FIP1L1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.1232
Q6ZSR9	0	0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.0000
Q8IUD2	23085	ERC1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.0000
Q8IZX4	138474	TAF1L	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q8ND56	26065	LSM14A	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1232
Q8WWM7	11273	ATXN2L	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.5044	0.4313
Q92541	23168	RTF1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.1232
Q92616	10985	GCN1L1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q92625	23294	ANKS1A	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.0000
Q92945	8570	KHSRP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1232

Q92994	2972	BRF1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q96BW1	139596	UPRT	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q96CP2	114984	FLYWCH2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q96QC0	5514	PPP1R10	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q99504	2140	EYA3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.2465
Q99962	6456	SH3GL2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q9BRS2	83732	RIOK1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q9BXF6	26056	RAB11FIP5	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1232
Q9H0B6	64837	KLC2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q9H2G2	9748	SLK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q9H6T3	79657	RPAP3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.1232
Q9H8H0	25926	NOL11	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1848
Q9HCS7	56949	XAB2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1848
Q9NPQ8	60626	RIC8A	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q9NRY4	2909	ARHGAP35	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.0000
Q9NTJ3	10051	SMC4	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q9NUY8	55773	TBC1D23	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q9NVM6	55192	DNAJC17	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q9UBB9	24144	TFIP11	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.4929
Q9UHD8	10801	SEPT9	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.6305	0.5545
Q9UK61	23272	FAM208A	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.0000
Q9UKE5	23043	TNIK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.0000
Q9UKV3	22985	ACIN1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.8197	1.2323
Q9UKV3-5	22985	ACIN1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.1848
Q9ULW0	22974	TPX2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.2465
Q9UNZ2	55968	NSFL1C	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1892	0.1848
Q9Y2J2	23136	EPB41L3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.1848
Q9Y2W1	9967	THRAP3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.4414	0.7394
Q9Y450	10767	HBS1L	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1261	0.1232
Q9Y5K6	23607	CD2AP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2522	0.6161
O00170	9049	AIP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
O00762	11065	UBE2C	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
O95219	8723	SNX4	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
O95793	6780	STAU1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
P04406	2597	GAPDH	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
P05455	6741	SSB	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
P11274	613	BCR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
P11940	26986	PABPC1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
P18669	5223	PGAM1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232

P20248	890	CCNA2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
P22626	3181	HNRNPA2B1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
P29084	2961	GTF2E2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
P46937	10413	YAP1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
P48643	22948	CCT5	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
P78347	2969	GTF2I	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2465
P78417	9446	GSTO1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
Q01968-2	4952	OCRL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q13185	11335	CBX3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q13200	5708	PSMD2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q14157	9898	UBAP2L	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2465
Q14157-1	9898	UBAP2L	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q14676	9656	MDC1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q15648	5469	MED1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q3V6T2	55704	CCDC88A	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q5T0N5	54874	FNBP1L	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q63HQ0	55435	AP1AR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q8NCF5	84901	NFATC2IP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
Q8ND82	55609	ZNF280C	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q8WUA2	85313	PPIL4	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q8WUF8	83989	FAM172A	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q92733	5546	PRCC	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
Q96GA3	84946	LTV1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q96I25	84991	RBM17	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.6778
Q96T58	23013	SPEN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
Q99460	5707	PSMD1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3081
Q9BRG1	84313	VPS25	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9C005	84661	DPY30	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9NS91	56852	RAD18	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2465
Q9NUQ8	55324	ABCF3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9NYZ3	51512	GTSE1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9P215	57645	POGK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9UHB6	51474	LIMA1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9UNH7	58533	SNX6	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9UPU5	23358	USP24	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232
Q9UPY3	23405	DICER1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
Q9Y2D5	11217	AKAP2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1848
Q9Y2S0	51082	POLR1D	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1232

Appendix C. Summary of MAM list revealed by MCS-ID for 24hrs labeling.

			#PSM					
UniProt	Entrez ID	Gene Name	MAM #1	MAM #2	OMM #1	OMM #2	ERM #1	ERM #2
O95292	9217	VAPB	23	26	4	2	28	23
P42167	7112	TMPO	10	13	10	6	79	64
Q14739	3930	LBR	5	6	3	1	59	49
Q7Z434	57506	MAVS	6	9	65	68	12	9
O15498	10652	YKT6	5	5	19	4	16	17
P50402	2010	EMD	4	5	13	3	37	24
O95721	9342	SNAP29	3	5	45	21	49	33
Q9NX40	54940	OCIAD1	4	5	28	21	1	3
O14737	9141	PDCD5	2	1	11	6	6	9
P37802	8407	TAGLN2	2	3	21	12	25	18
P51648	224	ALDH3A2	3	5	25	11	17	14
P60468	10952	SEC61B	9	5	4	1	24	49
P62820	5861	RAB1A	2	3	6	3	2	3
Q14318	23770	FKBP8	2	2	19	13	13	12
Q969Z3	54996	MARC2	3	3	13	6	2	2
Q96AG4	55379	LRRC59	3	3	2	2	16	21
Q99618	83461	CDCA3	2	1	3	2	3	3
Q9NZ45	55847	CISD1	3	2	9	8	2	1
O14979	9987	HNRNPDL	1	1	4	3	1	2
O15173	10424	PGRMC2	2	2	5	7	28	14
P13639	1938	EEF2	1	1	4	3	6	5
P13861	5576	PRKAR2A	1	1	17	16	1	3
P25685	3337	DNAJB1	1	1	5	5	1	2
P28288	5825	ABCD3	2	3	9	4	1	2
P46060	5905	RANGAP1	2	1	15	6	18	11
P46108	1398	CRK	1	2	15	2	4	2
P46109	1399	CRKL	1	1	10	5	7	11
P55010	1983	EIF5	1	2	12	6	18	10
P57105	55333	SYNJ2BP	1	2	10	1	1	2
Q14677	9685	CLINT1	1	1	48	38	24	24
Q15691	22919	MAPRE1	1	1	6	1	8	6
Q7Z2W4	56829	ZC3HAV1	1	3	22	8	13	10
Q8NC51	26135	SERBP1	1	3	8	4	8	10
Q96CS3	23197	FAF2	1	1	1	3	4	8
Q96EX1	113444	SMIM12	1	2	2	3	2	2

Q96JH7	80124	VCPIP1	1	1	6	6	3	2
Q96NC0	153527	ZMAT2	1	1	3	3	1	2
Q99733	4676	NAP1L4	1	2	22	12	5	7
Q9BQ61	79002	C19orf43	2	1	11	10	2	2
Q9BWH2	65991	FUNDC2	1	1	8	7	1	2
Q9H0L4	23283	CSTF2T	1	1	8	4	5	2
Q9H1E3	64710	NUCKS1	3	2	29	17	17	20
Q9H307	5411	PNN	1	1	24	14	5	1
Q9H3U1	55898	UNC45A	1	1	3	2	3	4
Q9H5V9	63932	CXorf56	2	1	3	3	3	3
Q9NR12	9260	PDLIM7	1	1	3	1	2	4
Q9NZC7	51741	WWOX	1	1	4	1	2	3
Q9Y5V3	9500	MAGED1	1	1	3	2	1	2
Q9Y6I9	51368	TEX264	3	3	2	1	11	8
Q8N4H5	401505	TOMM5	3	2	12	8	1	0
Q15388	9804	TOMM20	2	1	44	29	0	1
P15531	4830	NME1	1	1	6	6	0	1
Q5HYI7	345778	MTX3	1	1	9	7	0	0
Q96TC7	55177	RMDN3	1	5	2	1	0	1
Q9NVH0	55218	EXD2	1	4	4	2	0	0
Q9P0L0	9218	VAPA	7	8	0	0	26	37
Q5JTV8	26092	TOR1AIP1	3	3	1	0	19	21
Q96A33	57003	CCDC47	3	3	0	0	25	17
Q96S66	23155	CLCC1	3	5	0	0	19	27
O00264	10857	PGRMC1	2	3	0	1	26	15
O14683	9537	TP53I11	2	1	0	0	3	5
O75915	10550	ARL6IP5	2	1	0	0	8	6
P27824	821	CANX	2	1	0	0	7	9
Q15738	50814	NSDHL	2	3	0	0	9	10
Q8N4V1	93380	MMGT1	2	3	6	0	28	31
Q8N511	147007	TMEM199	3	3	0	0	8	7
Q8N5K1	493856	CISD2	2	1	0	0	4	6
Q96HY6	65992	DDRGK1	3	1	1	0	9	12
Q9H3N1	81542	TMX1	4	4	1	0	13	21
Q9UBM7	1717	DHCR7	2	1	0	0	6	6
O15155	10282	BET1	1	1	1	0	18	13
O75396	9554	SEC22B	2	2	0	0	9	6
O75694	9631	NUP155	1	2	0	0	4	7
O95210	8987	STBD1	1	1	0	0	3	6
O95873	57827	C6orf47	1	2	0	0	5	4

P05556	3688	ITGB1	1	3	0	0	4	5
P13797	5358	PLS3	1	2	3	0	2	4
P14625	7184	HSP90B1	1	1	4	0	4	5
P17706	5771	PTPN2	1	1	0	0	1	3
P29590	5371	PML	2	2	0	0	1	1
P30101	2923	PDIA3	1	1	0	0	2	6
P30519	3163	HMOX2	1	1	0	0	11	8
P43307	6745	SSR1	1	1	1	0	13	8
P63027	6844	VAMP2	1	1	5	0	2	4
Q5HYI8	285282	RABL3	1	1	2	0	5	2
Q5VV42	54901	CDKAL1	1	2	1	0	12	11
Q86UE4	92140	MTDH	2	6	0	0	68	54
Q8N5G2	55219	TMEM57	1	1	0	0	1	2
Q8NCS4	1.01E+08	ZMYM6NB	1	1	0	0	1	2
Q8TAA9	81839	VANGL1	1	1	0	0	3	3
Q8TCT9	81502	HM13	1	1	0	0	5	8
Q96A57	29058	TMEM230	2	2	0	0	5	4
Q96GC9	81671	VMP1	2	2	0	0	4	8
Q96JB5	80279	CDK5RAP3	1	1	1	0	2	1
Q96KC8	64215	DNAJC1	1	1	0	0	8	8
Q99614	7265	TTC1	2	1	3	0	1	2
Q9BW60	64834	ELOVL1	1	1	0	0	1	3
Q9BWL3	25912	C1orf43	1	1	0	0	5	7
Q9HC62	59343	SENP2	1	1	2	0	2	4
Q9NPA0	56851	EMC7	1	1	0	0	3	6
Q9NQ34	56674	TMEM9B	2	2	0	0	3	2
Q9NZ43	55850	USE1	1	3	0	0	15	16
Q9Y385	51465	UBE2J1	1	1	2	0	4	7
Q9Y5M8	58477	SRPRB	1	2	0	0	5	8
O14531	10570	DPYSL4	1	0	4	3	2	3
O43169	80777	CYB5B	2	0	9	8	5	4
O43639	8440	NCK2	1	0	3	1	2	4
O43768	2029	ENSA	1	0	7	7	7	9
P00338	3939	LDHA	1	0	4	1	2	1
P06748	4869	NPM1	1	0	121	89	6	11
P16333	4690	NCK1	1	0	3	1	2	3
P16949	3925	STMN1	1	0	13	9	12	17
P21333	2316	FLNA	1	0	7	8	8	4
Q92667	8165	AKAP1	1	0	33	28	3	1
Q9BXK5	23786	BCL2L13	1	0	10	13	2	1

Q9UH65	23075	SWAP70	1	0	2	2	5	2
Q9UHQ9	51706	CYB5R1	1	0	2	1	3	1
O94842	9878	TOX4	0	1	10	8	2	3
P00167	1528	CYB5A	0	2	8	7	14	9
P07737	5216	PFN1	0	2	9	8	12	8
P08238	3326	HSP90AB1	0	1	4	3	2	3
P19338	4691	NCL	0	1	77	43	4	9
P40855	5824	PEX19	0	1	13	7	1	3
P84077	375	ARF1	0	2	2	2	4	8
Q07812	581	BAX	0	1	4	3	2	4
Q13190	6811	STX5	0	1	2	1	7	6
Q13442	11333	PDAP1	0	1	4	1	4	5
Q5JRA6	375056	MIA3	0	1	5	1	13	16
Q5SQN1	116841	SNAP47	0	1	8	1	1	5
Q7Z6K5	348110	ARPIN	0	1	8	8	10	6
Q8IWZ8	57794	SUGP1	0	1	8	5	7	6
Q8N5I9	121053	C12orf45	0	1	9	4	2	4
Q8N6T3	55738	ARFGAP1	0	2	15	7	13	15
Q8NDI1	23301	EHBP1	0	1	2	2	6	8
Q96A49	94056	SYAP1	0	3	24	18	28	29
Q99640	9088	PKMYT1	0	2	5	2	4	5
Q9H444	128866	CHMP4B	0	1	2	1	4	7
Q9H501	51575	ESF1	0	1	2	1	1	2
Q9NR31	56681	SAR1A	0	1	1	3	2	5
Q9NZZ3	51510	CHMP5	0	2	7	5	13	7
Q9UH92	6945	MLX	0	1	4	2	2	3
Q9UHR5	29115	SAP30BP	0	1	6	1	3	4
Q9Y266	10726	NUDC	0	1	9	4	4	4
Q14008	9793	CKAP5	0	1	7	5	1	3
O00151	9124	PDLIM1	0	0	8	4	11	12
O00165	10456	HAX1	0	0	9	4	5	6
O00193	10944	SMAP	0	0	17	13	12	11
O00560	6386	SDCBP	0	0	4	1	6	5
O14562	56061	UBFD1	0	0	5	4	5	3
O14654	8471	IRS4	0	0	7	5	3	5
O14964	9146	HGS	0	0	4	1	1	4
O14976	2580	GAK	0	0	2	3	1	2
O15355	5496	PPM1G	0	0	13	3	1	1
O15541	7737	RNF113A	0	0	1	1	2	2
O43432	8672	EIF4G3	0	0	2	1	1	1

O43719	27336	HTATSF1	0	0	10	6	1	2
O60488	2182	ACSL4	0	0	2	1	2	2
O60664	10226	PLIN3	0	0	9	4	7	6
O60814	85236	HIST1H2BK	0	0	5	2	1	1
O75113	9683	N4BP1	0	0	2	1	1	2
O75179	26057	ANKRD17	0	0	4	4	1	1
O75410	6867	TACC1	0	0	4	2	8	10
O75937	22826	DNAJC8	0	0	10	3	3	5
O94888	26043	UBXN7	0	0	2	1	2	1
O95551	51567	TDP2	0	0	3	1	2	2
P00387	1727	CYB5R3	0	0	3	1	1	3
P00918	760	CA2	0	0	2	1	1	1
P04075	226	ALDOA	0	0	9	7	4	4
P05783	3875	KRT18	0	0	3	1	2	5
P06493	983	CDK1	0	0	5	1	5	4
P06730	1977	EIF4E	0	0	8	4	2	3
P08670	7431	VIM	0	0	6	4	6	6
P09234	6631	SNRPC	0	0	3	1	1	1
P09651	3178	HNRNPA1	0	0	2	3	2	2
P09661	6627	SNRPA1	0	0	11	9	7	2
P0DME0	646817	SETSIP	0	0	3	1	2	1
P13984	2963	GTF2F2	0	0	8	7	2	5
P14866	3191	HNRNPL	0	0	1	1	1	2
P15311	7430	EZR	0	0	1	1	4	2
P18583	6651	SON	0	0	1	2	1	1
P19532	7030	TFE3	0	0	4	1	1	1
P22061	5110	PCMT1	0	0	8	1	1	1
P22392	4831	NME2	0	0	5	1	1	3
P22626	3181	HNRNPA2B1	0	0	3	1	1	3
P23511	4800	NFYA	0	0	1	2	1	1
P23528	1072	CFL1	0	0	2	1	1	2
P25787	5683	PSMA2	0	0	1	1	1	1
P25789	5685	PSMA4	0	0	1	1	4	1
P27694	6117	RPA1	0	0	5	1	1	3
P27816	4134	MAP4	0	0	2	1	4	4
P29083	2960	GTF2E1	0	0	3	4	2	1
P30086	5037	PEBP1	0	0	1	2	1	1
P31948	10963	STIP1	0	0	2	2	5	4
P34931	3305	HSPA1L	0	0	4	2	4	4
P35244	6119	RPA3	0	0	1	1	1	1

P35637	2521	FUS	0	0	6	3	3	2
P35658	8021	NUP214	0	0	17	4	2	1
P35998	5701	PSMC2	0	0	4	3	3	2
P37840	6622	SNCA	0	0	3	1	1	5
P42224	6772	STAT1	0	0	2	2	3	1
P47755	830	CAPZA2	0	0	2	1	2	2
P49023	5829	PXN	0	0	1	3	1	3
P49321	4678	NASP	0	0	8	7	2	4
P49327	2194	FASN	0	0	4	5	6	6
P49588	16	AARS	0	0	2	1	1	1
P49792	5903	RANBP2	0	0	2	1	3	4
P49914	10588	MTHFS	0	0	3	3	2	3
P49959	4361	MRE11A	0	0	17	13	4	3
P50542	5830	PEX5	0	0	1	1	1	3
P50851	987	LRBA	0	0	1	2	2	1
P50990	10694	CCT8	0	0	12	9	14	15
P51149	7879	RAB7A	0	0	3	1	4	4
P51610	3054	HCFC1	0	0	12	7	1	3
P51617	3654	IRAK1	0	0	2	2	2	2
P51991	220988	HNRNPA3	0	0	3	2	3	3
P52272	4670	HNRNPM	0	0	10	5	2	3
P52594	3267	AGFG1	0	0	6	3	5	3
P52597	3185	HNRNPF	0	0	9	6	3	5
P52907	829	CAPZA1	0	0	4	2	4	3
P52948	4928	NUP98	0	0	2	6	11	8
P53999	10923	SUB1	0	0	5	3	2	2
P54652	3306	HSPA2	0	0	10	9	7	10
P55036	5710	PSMD4	0	0	7	3	4	2
P55081	4236	MFAP1	0	0	9	7	2	1
P55196	4301	MLLT4	0	0	3	1	4	2
P58876	3017	HIST1H2BD	0	0	1	1	1	1
P61247	6189	RPS3A	0	0	3	1	1	1
P61978	3190	HNRNPK	0	0	1	1	1	2
P78318	3476	IGBP1	0	0	2	2	5	4
P78344	1982	EIF4G2	0	0	14	3	3	4
Q00341	3069	HDLBP	0	0	1	1	4	5
Q00839	3192	HNRNPU	0	0	2	4	2	2
Q04637	1981	EIF4G1	0	0	9	7	6	9
Q07820	4170	MCL1	0	0	3	1	1	1
Q08211	1660	DHX9	0	0	6	3	1	2

Q13148	23435	TARDBP	0	0	6	4	2	3
Q13151	10949	HNRNPA0	0	0	5	2	1	4
Q13263	10155	TRIM28	0	0	7	6	5	3
Q13283	10146	G3BP1	0	0	1	2	2	4
Q13371	5082	PDCL	0	0	1	2	2	2
Q13428	6949	TCOF1	0	0	50	21	1	4
Q13501	8878	SQSTM1	0	0	3	1	5	3
Q13596	6642	SNX1	0	0	5	3	6	5
Q14157	9898	UBAP2L	0	0	13	6	2	3
Q14247	2017	CTTN	0	0	35	23	50	68
Q14320	9130	FAM50A	0	0	6	2	1	3
Q15003	23397	NCAPH	0	0	5	5	1	1
Q15025	10318	TNIP1	0	0	3	1	1	1
Q15042	22930	RAB3GAP1	0	0	1	1	6	4
Q15056	7458	EIF4H	0	0	6	3	6	4
Q15121	8682	PEA15	0	0	1	1	2	3
Q15233	4841	NONO	0	0	17	7	7	12
Q15287	10921	RNPS1	0	0	2	3	1	1
Q15366	5094	PCBP2	0	0	5	4	5	3
Q15417	1266	CNN3	0	0	7	5	13	18
Q15459	10291	SF3A1	0	0	6	5	1	3
Q15545	6879	TAF7	0	0	4	1	2	3
Q15555	10982	MAPRE2	0	0	3	2	4	4
Q15758	6510	SLC1A5	0	0	1	1	3	3
Q15843	4738	NEDD8	0	0	4	2	4	6
Q15942	7791	ZYX	0	0	9	2	4	8
Q32P51	144983	HNRNPA1L2	0	0	3	3	2	2
Q5T8P6	64062	RBM26	0	0	6	2	1	3
Q5VT66	64757	MARC1	0	0	4	1	2	1
Q5VTE0	0	EEF1A1P5	0	0	6	2	6	6
Q5VZ89	55667	DENND4C	0	0	8	2	2	3
Q6EEV6	387082	SUMO4	0	0	2	4	1	2
Q6IBS0	11344	TWF2	0	0	3	2	1	2
Q6P996	1.03E+08	PDXDC1	0	0	3	1	2	2
Q6PEY2	112714	TUBA3E	0	0	3	1	2	2
Q6PII3	51244	CCDC174	0	0	2	2	2	1
Q6PKG0	23367	LARP1	0	0	3	1	1	1
Q6PL24	283578	TMED8	0	0	5	4	5	4
Q6UN15	81608	FIP1L1	0	0	9	5	1	1
Q6Y7W6	26058	GIGYF2	0	0	3	1	2	1

Q6ZSR9	0		0	0	2	1	1	1
Q7L014	9879	DDX46	0	0	15	6	1	4
Q7Z4V5	84717	HDGFRP2	0	0	6	4	1	1
Q8IVW6	10620	ARID3B	0	0	9	4	1	2
Q8N6H7	84364	ARFGAP2	0	0	3	1	3	4
Q8N6N3	148423	C1orf52	0	0	8	8	5	8
Q8N7H5	54623	PAF1	0	0	5	3	1	1
Q8NBF2	374354	NHLRC2	0	0	2	1	1	1
Q8NBT2	147841	SPC24	0	0	4	3	3	1
Q8NCF5	84901	NFATC2IP	0	0	5	1	4	2
Q8ND82	55609	ZNF280C	0	0	3	3	1	1
Q8NFH5	129401	NUP35	0	0	4	2	3	4
Q8NFI4	0	ST13P5	0	0	2	1	2	3
Q8NI36	134430	WDR36	0	0	2	2	1	1
Q8WUX9	91782	CHMP7	0	0	3	1	4	7
Q8WW12	57092	PCNP	0	0	15	6	15	22
Q8WXF1	55269	PSPC1	0	0	6	2	1	2
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Q92541	23168	RTF1	0	0	7	3	1	1
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Q92733	5546	PRCC	0	0	4	3	1	1
Q92890	7353	UFD1L	0	0	4	2	3	1
Q92922	6599	SMARCC1	0	0	1	2	1	1
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Q93079	8345	HIST1H2BH	0	0	9	4	1	3
Q96AE4	8880	FUBP1	0	0	2	3	1	2
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Q96C19	79180	EFHD2	0	0	3	5	6	1
Q96D71	85021	REPS1	0	0	4	2	1	1
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Q96I24	8939	FUBP3	0	0	2	3	1	1
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Q96LB3	80173	IFT74	0	0	4	2	4	2
Q96MW1	124808	CCDC43	0	0	1	3	5	6
Q99426	1155	TBCB	0	0	6	2	1	1
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Q99961	6455	SH3GL1	0	0	1	1	3	3

Q9BV19	79078	C1orf50	0	0	3	1	3	1
Q9C037	89122	TRIM4	0	0	4	1	3	2
Q9C0C9	63893	UBE2O	0	0	2	2	3	1
Q9H3P7	64746	ACBD3	0	0	6	2	6	9
Q9H814	51808	PHAX	0	0	1	1	1	1
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Q9HB71	27101	CACYBP	0	0	8	3	2	1
Q9HCS7	56949	XAB2	0	0	2	2	1	1
Q9NPI6	55802	DCP1A	0	0	8	8	3	1
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Q9NRA8	56478	EIF4ENIF1	0	0	44	29	2	1
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Q9NX63	54927	CHCHD3	0	0	3	3	2	1
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Q9NYJ8	23118	TAB2	0	0	3	3	2	4
Q9P013	51503	CWC15	0	0	9	6	1	2
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Q9UEE9	10428	CFDP1	0	0	6	7	4	4
Q9UGP4	8994	LIMD1	0	0	4	1	4	3
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Q9UHV9	5202	PFDN2	0	0	1	1	1	2
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Q9UNZ2	55968	NSFL1C	0	0	3	2	7	8
Q9UPT8	23211	ZC3H4	0	0	1	1	1	1
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Q9Y2J2	23136	EPB41L3	0	0	4	1	1	2
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Q9Y3D7	51025	PAM16	0	0	2	1	1	1
Q9Y478	5564	PRKAB1	0	0	2	1	4	4
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P11021	3309	HSPA5	2	2	1	0	0	2
P61221	6059	ABCE1	1	1	0	0	0	0
P68104	1915	EEF1A1	1	1	0	0	0	0
Q15084	10130	PDIA6	1	1	1	0	0	2
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Q9Y2W6	11022	TDRKH	2	0	37	25	1	0
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Q9H425	84886	C1orf198	1	0	6	1	0	3
P38646	3313	HSPA9	0	1	6	2	0	0
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Q8TB36	54332	GDAP1	0	1	13	6	0	0
Q15050	23212	RRS1	0	1	3	4	0	0
O60238	665	BNIP3L	0	0	2	4	1	0
O60361	0	NME2P1	0	0	1	3	2	0
O75909	8812	CCNK	0	0	3	1	1	0
O95391	10569	SLU7	0	0	4	1	2	0
P10809	3329	HSPD1	0	0	5	1	2	0
P17844	1655	DDX5	0	0	4	5	2	0
P33240	1478	CSTF2	0	0	3	2	2	0
P61081	9040	UBE2M	0	0	2	1	1	0
Q00403	2959	GTF2B	0	0	1	1	1	0
Q13330	9112	MTA1	0	0	4	1	1	0
Q13573	22938	SNW1	0	0	12	5	1	0
Q13625	7159	TP53BP2	0	0	1	1	1	0
Q8IUD2	23085	ERC1	0	0	1	1	1	0
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Q96F63	90324	CCDC97	0	0	3	1	1	0
Q99627	10920	COPS8	0	0	1	1	3	0
Q9GZY8	56947	MFF	0	0	24	23	1	0
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Q9UPY3	23405	DICER1	0	0	1	1	2	0
Q9Y6M1	10644	IGF2BP2	0	0	1	1	1	0
O00221	4794	NFKBIE	0	0	1	1	0	1
O75528	10474	TADA3	0	0	3	3	0	1
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O77932	1797	DXO	0	0	1	1	0	1
O95202	3954	LETM1	0	0	10	3	0	1
P06737	5836	PYGL	0	0	2	1	0	2
P07910	3183	HNRNPC	0	0	3	2	0	1
P12236	293	SLC25A6	0	0	1	1	0	1
P12270	7175	TPR	0	0	7	5	0	2
P12956	2547	XRCC6	0	0	6	1	0	4
P15880	6187	RPS2	0	0	1	1	0	1
P18887	7515	XRCC1	0	0	1	1	0	1
P30613	5313	PKLR	0	0	2	2	0	1
P34897	6472	SHMT2	0	0	1	1	0	1
P35269	2962	GTF2F1	0	0	5	1	0	1
P39748	2237	FEN1	0	0	4	1	0	1
P52758	10247	HRSP12	0	0	6	7	0	1
P55265	103	ADAR	0	0	8	1	0	1
P78347	2969	GTF2I	0	0	12	2	0	1
P98175	8241	RBM10	0	0	2	1	0	2
Q04760	2739	GLO1	0	0	1	1	0	1
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Q13435	10992	SF3B2	0	0	16	13	0	3
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Q14980	4926	NUMA1	0	0	5	4	0	2
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Q86TB9	219988	PATL1	0	0	4	1	0	1
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Q8N257	128312	HIST3H2BB	0	0	2	1	0	1
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Q96A73	57179	KIAA1191	0	0	3	1	0	1
Q96DT6	84938	ATG4C	0	0	1	1	0	2
Q96EB1	26610	ELP4	0	0	2	1	0	2
Q9H8H0	25926	NOL11	0	0	3	3	0	1

Q9NS69	56993	TOMM22	0	0	1	3	0	1
Q9NZ09	51271	UBAP1	0	0	7	1	0	2
Q9NZI8	10642	IGF2BP1	0	0	1	1	0	2
Q9UIG0	9031	BAZ1B	0	0	2	1	0	1
Q9UK61	23272	FAM208A	0	0	3	1	0	1
O00429	10059	DNM1L	0	0	49	43	0	0
O00566	10199	MPHOSPH10	0	0	5	2	0	0
O15042	23350	U2SURP	0	0	1	1	0	0
O15119	6926	TBX3	0	0	1	2	0	0
O43395	9129	PRPF3	0	0	1	1	0	0
O43399	7165	TPD52L2	0	0	1	1	0	0
O43660	5356	PLRG1	0	0	2	1	0	0
O60264	8467	SMARCA5	0	0	3	2	0	0
O75376	9611	NCOR1	0	0	5	4	0	0
O75381	5195	PEX14	0	0	6	4	0	0
O75390	1431	CS	0	0	1	1	0	0
O75420	64599	GIGYF1	0	0	2	1	0	0
O75643	23020	SNRNP200	0	0	1	2	0	0
O75683	6838	SURF6	0	0	8	3	0	0
O95684	11116	FGFR1OP	0	0	4	1	0	0
O95831	9131	AIFM1	0	0	3	2	0	0
O96008	10452	TOMM40	0	0	2	1	0	0
P00505	2806	GOT2	0	0	1	1	0	0
P06576	506	ATP5B	0	0	20	15	0	0
P11274	613	BCR	0	0	1	1	0	0
P11586	4522	MTHFD1	0	0	9	10	0	0
P20671	3013	HIST1H2AD	0	0	3	3	0	0
P21796	7416	VDAC1	0	0	3	1	0	0
P23246	6421	SFPQ	0	0	1	1	0	0
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P36578	6124	RPL4	0	0	3	1	0	0
P38432	8161	COIL	0	0	9	2	0	0
P39880	1523	CUX1	0	0	3	2	0	0
P40939	3030	HADHA	0	0	2	2	0	0
P43243	9782	MATR3	0	0	9	3	0	0
P43246	4436	MSH2	0	0	1	1	0	0
P48436	6662	SOX9	0	0	2	2	0	0
P48634	7916	PRRC2A	0	0	4	3	0	0
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P52756	10181	RBM5	0	0	1	1	0	0

Q08378	2802	GOLGA3	0	0	4	1	0	0
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Q13823	29889	GNL2	0	0	1	1	0	0
Q15020	9733	SART3	0	0	5	1	0	0
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Q5TC12	64756	ATPAF1	0	0	4	1	0	0
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Q8IWX8	10523	CHERP	0	0	1	1	0	0
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Q8NBZ0	283899	INO80E	0	0	1	1	0	0
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Q8TCU4	7840	ALMS1	0	0	7	2	0	0
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Q8TEH3	57706	DENND1A	0	0	2	1	0	0
Q8WUZ0	9274	BCL7C	0	0	1	1	0	0
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Q92540	9887	SMG7	0	0	3	1	0	0
Q92844	10010	TANK	0	0	5	1	0	0
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Q96DX7	54765	TRIM44	0	0	1	1	0	0
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Q9BVP2	26354	GNL3	0	0	2	1	0	0
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Q9NVU7	55153	SDAD1	0	0	2	1	0	0
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Q9Y2W2	51729	WBP11	0	0	13	2	0	0
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O75787	10159	ATP6AP2	1	0	0	0	1	1
P84157	439921	MXRA7	1	0	1	0	29	22
Q07065	10970	CKAP4	1	0	0	0	11	16
Q8TCJ2	201595	STT3B	1	0	0	0	4	5
Q9HDC5	56704	JPH1	1	0	0	0	4	3
Q9NYM9	51272	BET1L	1	0	0	0	4	3
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O14668	5638	PRRG1	0	1	0	0	4	3
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P09601	3162	HMOX1	0	1	0	0	1	4
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P60709	60	ACTB	0	1	1	0	3	4
Q53FV1	29095	ORMDL2	0	1	0	0	1	1
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Q8N183	91942	NDUFAF2	0	1	0	0	3	3
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Q9Y2S6	51372	TMA7	0	1	0	0	1	1
A0FGR8	57488	ESYT2	0	0	0	0	7	4
A6NKD9	317762	CCDC85C	0	0	8	0	1	1
A8CG34	0	POM121C	0	0	0	0	2	1
O00154	11332	ACOT7	0	0	0	0	1	1
O00273	1676	DFFA	0	0	2	0	4	2
O00400	9197	SLC33A1	0	0	0	0	12	8
O00425	10643	IGF2BP3	0	0	1	0	1	1
O00559	9166	EBAG9	0	0	0	0	2	1

O00750	5287	PIK3C2B	0	0	2	0	1	1
O00762	11065	UBE2C	0	0	1	0	1	1
O00767	6319	SCD	0	0	0	0	1	1
O14523	9854	C2CD2L	0	0	0	0	4	5
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O14639	3983	ABLIM1	0	0	0	0	1	2
O14653	9570	GOSR2	0	0	0	0	1	2
O14681	9538	EI24	0	0	0	0	3	5
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O14828	10067	SCAMP3	0	0	0	0	1	1
O15027	9919	SEC16A	0	0	1	0	5	6
O15084	23243	ANKRD28	0	0	0	0	1	2
O15144	10109	ARPC2	0	0	0	1	1	1
O15269	10558	SPTLC1	0	0	0	0	2	3
O15320	4253	CTAGE5	0	0	0	0	1	2
O15371	8664	EIF3D	0	0	0	0	1	2
O15504	11097	NUPL2	0	0	0	0	2	3
O43318	6885	MAP3K7	0	0	0	0	1	2
O43396	9352	TXNL1	0	0	0	0	1	2
O43447	10465	PPIH	0	0	1	0	4	1
O43491	2037	EPB41L2	0	0	1	0	1	2
O43505	11041	B4GAT1	0	0	0	0	1	1
O43741	5565	PRKAB2	0	0	0	0	1	1
O43752	10228	STX6	0	0	0	0	2	3
O43809	11051	NUDT21	0	0	2	0	1	3
O60443	1687	DFNA5	0	0	0	0	2	2
O60493	8724	SNX3	0	0	0	0	6	3
O60499	8677	STX10	0	0	0	0	4	1
O60566	701	BUB1B	0	0	1	0	1	1
O60684	23633	KPNA6	0	0	0	0	1	1
O60749	6643	SNX2	0	0	1	0	4	5
O60763	8615	USO1	0	0	0	0	1	3
O60784	10043	TOM1	0	0	0	0	1	1
O60831	11230	PRAF2	0	0	0	0	3	2
O60869	8721	EDF1	0	0	1	0	1	4
O75116	9475	ROCK2	0	0	0	0	1	1
O75143	9776	ATG13	0	0	0	0	1	1
O75379	8674	VAMP4	0	0	0	0	2	3
O75427	4034	LRCH4	0	0	0	0	1	1
O75534	7812	CSDE1	0	0	1	0	3	6

O75581	4040	LRP6	0	0	0	0	1	1
O75674	10040	TOM1L1	0	0	0	0	1	1
O75792	10535	RNASEH2A	0	0	1	0	3	4
O75794	8872	CDC123	0	0	0	0	2	3
O75821	8666	EIF3G	0	0	0	0	1	2
O75844	10269	ZMPSTE24	0	0	0	0	6	6
O75874	3417	IDH1	0	0	0	2	1	1
O75886	10254	STAM2	0	0	1	0	2	1
O75976	1362	CPD	0	0	0	0	1	1
O76024	7466	WFS1	0	0	0	0	3	1
O76094	6731	SRP72	0	0	1	0	2	1
O94830	23259	DDHD2	0	0	0	0	1	1
O94874	23376	UFL1	0	0	0	0	3	4
O94901	23353	SUN1	0	0	0	0	1	2
O94929	22885	ABLIM3	0	0	0	0	1	1
O94991	26050	SLITRK5	0	0	0	0	1	1
O95197	10313	RTN3	0	0	0	0	2	4
O95218	9406	ZRANB2	0	0	9	0	4	4
O95219	8723	SNX4	0	0	1	0	1	1
O95249	9527	GOSR1	0	0	3	0	4	5
O95372	11313	LYPLA2	0	0	2	0	3	1
O95373	10527	IPO7	0	0	0	1	1	5
O95433	10598	AHSA1	0	0	2	0	6	3
O95573	2181	ACSL3	0	0	0	0	2	3
O95630	10617	STAMBP	0	0	0	0	3	2
O95816	9532	BAG2	0	0	0	0	1	4
O95905	11319	ECD	0	0	1	0	1	1
O96005	1209	CLPTM1	0	0	0	0	2	4
P00374	1719	DHFR	0	0	0	0	2	1
P00492	3251	HPRT1	0	0	1	0	1	1
P02545	4000	LMNA	0	0	0	0	1	2
P04035	3156	HMGCR	0	0	0	0	1	1
P04406	2597	GAPDH	0	0	1	0	5	3
P04792	3315	HSPB1	0	0	0	0	1	1
P05023	476	ATP1A1	0	0	0	0	2	1
P05141	292	SLC25A5	0	0	0	0	2	1
P05198	1965	EIF2S1	0	0	0	0	1	1
P06213	3643	INSR	0	0	0	0	2	2
P06733	2023	ENO1	0	0	1	0	5	6
P07195	3945	LDHB	0	0	3	0	2	1

P07197	4741	NEFM	0	0	1	0	1	3
P07355	302	ANXA2	0	0	0	0	2	1
P07437	203068	TUBB	0	0	1	0	2	1
P08195	6520	SLC3A2	0	0	0	0	6	4
P08237	5213	PFKM	0	0	1	0	1	1
P08240	6734	SRPRA	0	0	0	0	7	11
P08243	440	ASNS	0	0	2	0	2	2
P09497	1212	CLTB	0	0	1	0	1	1
P0DMV9	3303	HSPA1B	0	0	1	0	2	2
P10398	369	ARAF	0	0	0	0	1	1
P10636	4137	MAPT	0	0	0	0	1	1
P11142	3312	HSPA8	0	0	1	0	1	4
P11171	2035	EPB41	0	0	1	0	3	1
P11717	3482	IGF2R	0	0	0	0	3	3
P11940	26986	PABPC1	0	0	2	0	2	1
P12277	1152	CKB	0	0	2	0	2	1
P15259	5224	PGAM2	0	0	2	0	3	1
P15927	6118	RPA2	0	0	0	0	1	1
P16152	873	CBR1	0	0	1	0	1	1
P16435	5447	POR	0	0	0	0	8	8
P16615	488	ATP2A2	0	0	0	0	3	4
P17302	2697	GJA1	0	0	0	0	1	1
P17980	5702	PSMC3	0	0	0	0	1	1
P18031	5770	PTPN1	0	0	0	1	2	6
P18206	7414	VCL	0	0	0	0	1	1
P20020	490	ATP2B1	0	0	0	0	2	2
P20290	689	BTF3	0	0	2	0	3	3
P20340	5870	RAB6A	0	0	2	0	1	1
P20618	5689	PSMB1	0	0	0	0	2	1
P20700	4001	LMNB1	0	0	0	0	13	10
P21964	1312	COMT	0	0	0	0	3	1
P22102	2618	GART	0	0	0	0	1	1
P22234	10606	PAICS	0	0	4	0	2	5
P23443	6198	RPS6KB1	0	0	1	0	1	1
P23588	1975	EIF4B	0	0	2	0	5	4
P23634	493	ATP2B4	0	0	0	0	2	2
P24534	1933	EEF1B2	0	0	1	0	5	3
P25098	156	ADRBK1	0	0	0	0	2	2
P26196	1656	DDX6	0	0	0	0	2	1
P27544	10715	CERS1	0	0	0	0	2	1

P29966	4082	MARCKS	0	0	0	0	1	1
P30044	25824	PRDX5	0	0	2	0	1	2
P30419	4836	NMT1	0	0	0	0	3	1
P30520	159	ADSS	0	0	0	0	1	1
P31350	6241	RRM2	0	0	0	0	2	2
P31689	3301	DNAJA1	0	0	3	0	4	2
P31939	471	ATIC	0	0	1	0	2	3
P32322	5831	PYCR1	0	0	0	0	1	1
P35520	1.03E+08	CBS	0	0	1	0	1	1
P35606	9276	COPB2	0	0	0	0	1	4
P35610	6646	SOAT1	0	0	0	0	4	4
P36405	403	ARL3	0	0	0	0	1	1
P36639	4521	NUDT1	0	0	0	0	1	1
P36873	5501	PPP1CC	0	0	0	0	1	1
P41208	1069	CETN2	0	0	0	0	1	1
P41227	8260	NAA10	0	0	0	0	1	2
P42166	7112	TMPO	0	0	1	0	10	11
P43121	4162	MCAM	0	0	0	0	1	1
P43487	5902	RANBP1	0	0	6	0	5	12
P46379	7917	BAG6	0	0	0	0	2	1
P46821	4131	MAP1B	0	0	0	0	2	2
P46937	10413	YAP1	0	0	0	2	1	1
P47914	6159	RPL29	0	0	0	0	1	2
P48426	5305	PIP4K2A	0	0	0	0	1	1
P48444	372	ARCN1	0	0	0	0	3	5
P48729	1452	CSNK1A1	0	0	0	0	1	3
P49189	223	ALDH9A1	0	0	0	0	2	1
P49755	10972	TMED10	0	0	0	0	1	1
P49768	5663	PSEN1	0	0	0	0	1	1
P49773	3094	HINT1	0	0	3	0	5	6
P49790	9972	NUP153	0	0	0	3	8	13
P50747	3141	HLCS	0	0	1	0	3	2
P50991	10575	CCT4	0	0	0	0	1	1
P51397	1611	DAP	0	0	0	0	1	3
P51452	1845	DUSP3	0	0	1	0	3	2
P51572	10134	BCAP31	0	0	1	0	22	27
P51795	1184	CLCN5	0	0	0	1	2	1
P51809	6845	VAMP7	0	0	0	0	1	1
P51858	3068	HDGF	0	0	3	0	1	1
P52429	8526	DGKE	0	0	0	0	1	2

P52565	396	ARHGDIA	0	0	0	0	4	5
P53367	27236	ARFIP1	0	0	0	0	2	4
P53618	1315	COPB1	0	0	0	0	1	2
P53621	1314	COPA	0	0	0	0	1	2
P53794	0	SLC5A3	0	0	0	0	1	1
P53801	754	PTTG1IP	0	0	0	0	1	3
P54252	4287	ATXN3	0	0	0	0	2	1
P54577	8565	YARS	0	0	3	0	2	3
P54707	479	ATP12A	0	0	0	0	1	1
P54727	5887	RAD23B	0	0	0	0	2	4
P55209	4673	NAP1L1	0	0	0	0	1	1
P55211	842	CASP9	0	0	0	0	1	1
P55795	3188	HNRNPH2	0	0	0	0	1	1
P56211	10776	ARPP19	0	0	3	0	2	5
P56937	51478	HSD17B7	0	0	0	0	1	1
P58004	83667	SESN2	0	0	0	0	1	1
P60228	3646	EIF3E	0	0	0	0	1	1
P60842	1973	EIF4A1	0	0	0	0	2	3
P60866	6224	RPS20	0	0	0	0	1	1
P61011	6729	SRP54	0	0	0	0	5	5
P61024	1163	CKS1B	0	0	0	0	1	1
P61077	7323	UBE2D3	0	0	0	0	1	1
P61106	51552	RAB14	0	0	0	0	1	1
P61244	4149	MAX	0	0	2	0	1	2
P61326	4116	MAGOH	0	0	1	0	1	2
P61769	567	B2M	0	0	0	0	1	1
P61923	22818	COPZ1	0	0	3	0	5	5
P61956	6613	SUMO2	0	0	2	0	2	2
P61960	51569	UFM1	0	0	0	0	2	3
P61970	10204	NUTF2	0	0	0	0	1	1
P62136	5499	PPP1CA	0	0	0	1	1	2
P62258	7531	YWHAE	0	0	0	0	2	1
P62330	382	ARF6	0	0	2	0	2	1
P62491	8766	RAB11A	0	0	0	1	2	1
P62826	5901	RAN	0	0	1	0	1	1
P62841	6209	RPS15	0	0	0	0	1	1
P62937	5478	PPIA	0	0	2	0	3	6
P63241	1984	EIF5A	0	0	0	0	3	1
P67870	1460	CSNK2B	0	0	4	0	1	3
P67936	7171	TPM4	0	0	0	0	1	1

P78310	1525	CXADR	0	0	0	0	1	1
P78536	6868	ADAM17	0	0	0	0	4	5
P83731	6152	RPL24	0	0	0	0	1	4
P98170	331	XIAP	0	0	1	0	3	4
Q00765	7905	REEP5	0	0	0	0	9	9
Q01813	5214	PFKP	0	0	0	0	1	2
Q01814	491	ATP2B2	0	0	0	0	2	2
Q01968	4952	OCRL	0	0	0	0	1	2
Q02790	2288	FKBP4	0	0	1	0	1	3
Q02878	6128	RPL6	0	0	2	0	1	2
Q03252	84823	LMNB2	0	0	0	0	4	6
Q04323	51035	UBXN1	0	0	0	0	5	9
Q04721	4853	NOTCH2	0	0	0	0	2	1
Q04917	7533	YWHAH	0	0	0	1	3	1
Q05084	3382	ICA1	0	0	0	0	2	1
Q05682	800	CALD1	0	0	2	0	1	4
Q06481	334	APLP2	0	0	0	0	1	1
Q06830	5052	PRDX1	0	0	2	0	2	1
Q07960	392	ARHGAP1	0	0	3	0	11	4
Q09666	79026	AHNAK	0	0	1	0	3	1
Q0GE19	84068	SLC10A7	0	0	0	0	1	2
Q12772	6721	SREBF2	0	0	0	0	1	1
Q12797	444	ASPH	0	0	0	0	1	2
Q12893	11070	TMEM115	0	0	0	0	2	2
Q12959	1739	DLG1	0	0	1	0	1	2
Q12981	662	BNIP1	0	0	0	0	8	3
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Q13177	5062	PAK2	0	0	0	0	1	3
Q13185	11335	CBX3	0	0	0	0	1	2
Q13308	5754	PTK7	0	0	0	0	2	1
Q13347	8668	EIF3I	0	0	0	1	3	4
Q13370	5140	PDE3B	0	0	0	0	1	1
Q13505	4580	MTX1	0	0	0	4	2	3
Q13526	5300	PIN1	0	0	0	0	1	1
Q13572	3705	ITPK1	0	0	1	0	1	2
Q13586	6786	STIM1	0	0	0	0	19	21
Q13765	4666	NACA	0	0	2	0	4	2
Q13951	865	CBFB	0	0	0	0	1	1
Q14011	1153	CIRBP	0	0	1	0	1	1
Q14126	1829	DSG2	0	0	0	0	5	7

Q14160	23513	SCRIB	0	0	0	0	1	1
Q14353	2593	GAMT	0	0	1	0	1	1
Q14498	9584	RBM39	0	0	1	0	1	2
Q14571	3709	ITPR2	0	0	0	0	1	1
Q14596	4077	NBR1	0	0	0	1	1	2
Q14697	23193	GANAB	0	0	0	0	1	2
Q14789	2804	GOLGB1	0	0	0	0	2	2
Q14847	3927	LASP1	0	0	0	0	6	5
Q14BN4	7871	SLMAP	0	0	0	0	2	3
Q15005	9789	SPCS2	0	0	0	0	8	5
Q15008	9861	PSMD6	0	0	0	0	1	1
Q15011	9709	HERPUD1	0	0	0	0	4	4
Q15036	9784	SNX17	0	0	0	0	1	1
Q15051	9657	IQCB1	0	0	1	0	1	1
Q15126	10654	PMVK	0	0	0	0	1	1
Q15185	10728	PTGES3	0	0	0	0	1	2
Q15365	5093	PCBP1	0	0	3	0	1	2
Q15464	6461	SHB	0	0	0	0	1	2
Q15629	23471	TRAM1	0	0	0	0	1	1
Q15750	10454	TAB1	0	0	0	0	1	1
Q16527	1466	CSRP2	0	0	0	0	2	3
Q16625	1.01E+08	OCLN	0	0	0	0	3	2
Q16799	6252	RTN1	0	0	0	0	7	6
Q16850	1595	CYP51A1	0	0	0	0	2	4
Q2TAL8	54870	QRICH1	0	0	1	0	1	1
Q3MHD2	124801	LSM12	0	0	2	0	2	2
Q4KMQ2	196527	ANO6	0	0	0	0	2	1
Q53FP2	59353	TMEM35	0	0	0	0	1	1
Q53GS7	2733	GLE1	0	0	0	0	1	1
Q562R1	345651	ACTBL2	0	0	1	0	1	1
Q5JSH3	54521	WDR44	0	0	0	0	4	6
Q5T8D3	91452	ACBD5	0	0	3	0	1	2
Q5T9L3	79971	WLS	0	0	0	0	1	2
Q5VWZ2	127018	LYPLAL1	0	0	0	1	4	2
Q629K1	286144	TRIQK	0	0	0	0	3	4
Q658Y4	157769	FAM91A1	0	0	0	0	3	2
Q68DQ2	131544	CRYBG3	0	0	3	0	1	1
Q6EEV4	81488	POLR2M	0	0	3	0	1	2
Q6FI81	57019	CIAPIN1	0	0	2	0	1	2
Q6FIF0	54469	ZFAND6	0	0	1	0	1	1

Q6IC98	23151	GRAMD4	0	0	0	0	1	2
Q6NUQ1	60561	RINT1	0	0	0	0	1	3
Q6NUQ4	54867	TMEM214	0	0	0	0	5	7
Q6P1M0	10999	SLC27A4	0	0	0	0	2	4
Q6P1N0	54862	CC2D1A	0	0	0	0	1	1
Q6P6B1	203111	ERICH5	0	0	1	0	1	2
Q6P9B6	57707	TLDC1	0	0	0	0	1	1
Q6T4P5	79948	PLPPR3	0	0	0	0	1	1
Q6UUV9	23373	CRTC1	0	0	1	0	1	1
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Q6ZNB6	152518	NFXL1	0	0	0	0	1	4
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Q6ZVM7	146691	TOM1L2	0	0	1	0	3	4
Q70UQ0	121457	IKBIP	0	0	0	0	2	3
Q71RG4	79089	TMUB2	0	0	0	0	2	1
Q7KYR7	11120	BTN2A1	0	0	0	0	1	1
Q7KZF4	27044	SND1	0	0	1	0	5	4
Q7Z2Z2	79631	EFL1	0	0	0	0	1	1
Q7Z3D4	116068	LYSMD3	0	0	0	0	4	1
Q7Z4G4	60487	TRMT11	0	0	0	0	1	1
Q7Z569	8315	BRAP	0	0	0	1	3	2
Q7Z5L2	27291	R3HCC1L	0	0	1	0	1	1
Q86TM6	84447	SYVN1	0	0	0	0	1	1
Q86UL3	137964	GPAT4	0	0	0	0	1	2
Q86UP2	3895	KTN1	0	0	0	0	19	20
Q86V24	79602	ADIPOR2	0	0	0	0	1	2
Q86W56	670	PARG	0	0	0	0	1	1
Q86XL3	23141	ANKLE2	0	0	1	0	8	15
Q86XP3	11325	DDX42	0	0	1	0	3	2
Q86Y82	23673	STX12	0	0	0	0	1	2
Q8IV38	57037	ANKMY2	0	0	0	0	1	1
Q8IXW5	79871	RPAP2	0	0	1	0	2	2
Q8IZJ1	219699	UNC5B	0	0	0	0	1	1
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Q8N0Y7	441531	PGAM4	0	0	0	0	1	2
Q8N573	55074	OXR1	0	0	0	0	1	1
Q8N6S5	151188	ARL6IP6	0	0	0	0	2	4
Q8NC96	25977	NECAP1	0	0	0	0	1	1
Q8NE01	26505	CNNM3	0	0	0	0	1	2
Q8NEL9	80821	DDHD1	0	0	2	0	1	1

Q8NEN9	118987	PDZD8	0	0	0	0	10	13
Q8NF91	23345	SYNE1	0	0	1	0	2	3
Q8NFH3	348995	NUP43	0	0	0	0	1	1
Q8NFQ8	163590	TOR1AIP2	0	0	0	0	3	7
Q8NHP6	158747	MOSPD2	0	0	0	0	1	1
Q8TBA6	9950	GOLGA5	0	0	2	0	5	6
Q8TCD1	497661	C18orf32	0	0	0	0	1	4
Q8TEM1	23225	NUP210	0	0	0	0	1	1
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Q8WU90	55854	ZC3H15	0	0	0	0	1	3
Q8WUM0	55746	NUP133	0	0	0	1	7	3
Q8WVM8	23256	SCFD1	0	0	2	0	10	8
Q8WWM7	11273	ATXN2L	0	0	4	0	3	2
Q8WXH0	23224	SYNE2	0	0	0	0	8	7
Q8WYP5	25909	AHCTF1	0	0	0	0	2	1
Q92499	1653	DDX1	0	0	0	0	1	1
Q92545	23505	TMEM131	0	0	0	0	2	1
Q92572	1176	AP3S1	0	0	1	0	1	1
Q92609	9779	TBC1D5	0	0	0	0	1	1
Q92870	323	APBB2	0	0	1	0	1	1
Q92953	9312	KCNB2	0	0	0	0	1	2
Q96AT1	57456	KIAA1143	0	0	0	0	1	6
Q96AT9	6120	RPE	0	0	1	0	2	1
Q96BZ9	128637	TBC1D20	0	0	0	0	5	4
Q96E16	114926	SMIM19	0	0	0	0	12	3
Q96GQ5	64755	C16orf58	0	0	0	0	1	2
Q96H20	11267	SNF8	0	0	0	0	1	1
Q96HA1	9883	POM121	0	0	0	0	2	3
Q96HC4	10611	PDLIM5	0	0	5	0	3	4
Q96HR9	92840	REEP6	0	0	0	0	1	1
Q96IG2	84961	FBXL20	0	0	0	0	1	1
Q96K49	84910	TMEM87B	0	0	0	0	1	1
Q96KA5	81037	CLPTM1L	0	0	0	0	1	1
Q96KB5	55872	PBK	0	0	0	0	1	1
Q96KN1	157638	FAM84B	0	0	0	0	1	3
Q96LT7	203228	C9orf72	0	0	1	0	2	2
Q96M27	133619	PRRC1	0	0	1	0	1	1
Q96NT0	84317	CCDC115	0	0	0	0	3	3
Q96P70	55705	IPO9	0	0	1	0	1	1
Q96PZ0	54517	PUS7	0	0	3	0	1	2

Q96QD8	54407	SLC38A2	0	0	0	0	2	2
Q96RE7	112939	NACC1	0	0	0	0	1	1
Q96RU3	23048	FNBP1	0	0	0	0	1	1
Q96SK2	84928	TMEM209	0	0	1	0	8	6
Q99504	2140	EYA3	0	0	2	0	1	1
Q99590	9169	SCAF11	0	0	0	0	1	1
Q99615	7266	DNAJC7	0	0	0	0	2	1
Q99623	11331	PHB2	0	0	1	0	1	3
Q99675	10668	CGRRF1	0	0	0	0	1	1
Q99942	6048	RNF5	0	0	0	0	1	3
Q99962	6456	SH3GL2	0	0	0	0	1	1
Q9BQA1	79084	WDR77	0	0	0	0	1	1
Q9BQE4	55829	VIMP	0	0	0	0	7	6
Q9BQE5	23780	APOL2	0	0	0	0	3	1
Q9BRG1	84313	VPS25	0	0	0	0	2	1
Q9BRX2	53918	PELO	0	0	0	0	1	1
Q9BSJ8	23344	ESYT1	0	0	0	0	15	13
Q9BSW2	84766	CRACR2A	0	0	1	0	1	1
Q9BTX1	55706	NDC1	0	0	0	0	9	7
Q9BUK6	55154	MSTO1	0	0	0	0	3	3
Q9BUV8	55969	C20orf24	0	0	0	0	1	1
Q9BV40	8673	VAMP8	0	0	0	0	4	2
Q9BVT8	83590	TMUB1	0	0	0	0	1	2
Q9BW91	53343	NUDT9	0	0	0	0	1	1
Q9BXB4	114885	OSBPL11	0	0	0	0	3	5
Q9BZF1	114882	OSBPL8	0	0	0	0	5	4
Q9C0B1	79068	FTO	0	0	0	0	1	1
Q9C0C4	54910	SEMA4C	0	0	0	0	1	1
Q9C0E8	80856	LNP	0	0	0	0	13	10
Q9GZM5	25844	YIPF3	0	0	0	0	1	2
Q9GZT9	54583	EGLN1	0	0	0	1	1	2
Q9H0A8	54939	COMMD4	0	0	0	0	1	1
Q9H267	26276	VPS33B	0	0	0	0	1	5
Q9H2G2	9748	SLK	0	0	1	0	1	1
Q9H2J4	79031	PDCL3	0	0	0	0	1	1
Q9H2J7	55117	SLC6A15	0	0	0	0	4	3
Q9H2M9	25782	RAB3GAP2	0	0	0	0	3	5
Q9H2P9	51611	DPH5	0	0	0	0	1	2
Q9H467	79004	CUEDC2	0	0	2	0	2	1
Q9H6H4	80346	REEP4	0	0	0	0	1	2

Q9H6K1	64771	C6orf106	0	0	0	0	1	1
Q9H6T3	79657	RPAP3	0	0	1	0	2	1
Q9H6U8	79796	ALG9	0	0	0	0	4	6
Q9H8M9	84141	EVA1A	0	0	0	0	1	1
Q9H8Y8	26003	GORASP2	0	0	0	0	2	3
Q9H902	65055	REEP1	0	0	0	0	2	1
Q9HAP2	22877	MLXIP	0	0	0	0	1	1
Q9HB21	59338	PLEKHA1	0	0	0	0	2	1
Q9HBM0	55591	VEZT	0	0	0	0	7	4
Q9HBZ2	9915	ARNT2	0	0	0	0	1	2
Q9HC07	55858	TMEM165	0	0	0	0	1	1
Q9HCM3	57670	KIAA1549	0	0	0	0	1	1
Q9HCN4	11321	GPN1	0	0	0	0	2	2
Q9HCU5	10113	PREB	0	0	3	0	3	5
Q9HD42	5119	CHMP1A	0	0	0	0	1	3
Q9NP61	26286	ARFGAP3	0	0	4	0	4	8
Q9NP72	22931	RAB18	0	0	0	0	2	2
Q9NP73	79868	ALG13	0	0	1	0	2	2
Q9NQ29	55692	LUC7L	0	0	0	0	1	1
Q9NQC3	57142	RTN4	0	0	0	0	6	7
Q9NQC7	1540	CYLD	0	0	0	0	1	1
Q9NRG9	8086	AAAS	0	0	1	0	4	4
Q9NRV9	50865	HEBP1	0	0	0	0	1	1
Q9NRY5	10827	FAM114A2	0	0	2	0	3	6
Q9NSA3	56998	CTNNBIP1	0	0	2	0	3	3
Q9NT62	64422	ATG3	0	0	0	0	4	3
Q9NTJ3	10051	SMC4	0	0	1	0	1	1
Q9NUP9	55327	LIN7C	0	0	0	0	1	2
Q9NVZ3	55707	NECAP2	0	0	3	0	1	3
Q9NW68	55108	BSDC1	0	0	1	0	1	1
Q9NWV4	54987	C1orf123	0	0	1	0	2	3
Q9NWV8	29086	BABAM1	0	0	0	0	3	1
Q9NX08	54951	COMMD8	0	0	0	0	1	1
Q9NX61	54929	TMEM161A	0	0	0	0	2	2
Q9NXB9	54898	ELOVL2	0	0	0	0	2	3
Q9NXW2	54788	DNAJB12	0	0	0	0	2	2
Q9NZ32	55860	ACTR10	0	0	0	0	1	1
Q9NZQ3	51517	NCKIPSD	0	0	0	0	1	2
Q9P0S3	94101	ORMDL1	0	0	0	0	2	3
Q9P0U3	29843	SENP1	0	0	0	0	1	1

Q9P246	57620	STIM2	0	0	0	0	1	3
Q9P2E9	6238	RRBP1	0	0	0	0	4	4
Q9P2W9	53407	STX18	0	0	1	0	11	11
Q9UEU0	10490	VTI1B	0	0	1	0	3	2
Q9UGP8	11231	SEC63	0	0	0	0	11	10
Q9UH99	25777	SUN2	0	0	0	0	1	2
Q9UHD1	26973	CHORDC1	0	0	0	0	2	2
Q9UHD8	10801	SEPT9	0	0	3	0	1	2
Q9UI14	10567	RABAC1	0	0	0	0	2	2
Q9UI30	51504	TRMT112	0	0	2	0	2	6
Q9UK45	51690	LSM7	0	0	0	0	1	1
Q9UKK9	11164	NUDT5	0	0	2	0	2	3
Q9UKT5	26272	FBXO4	0	0	0	0	1	1
Q9UKY7	55573	CDV3	0	0	4	0	5	8
Q9UL25	23011	RAB21	0	0	1	0	1	1
Q9ULH0	57498	KIDINS220	0	0	0	0	2	2
Q9UM00	54499	TMCO1	0	0	0	0	1	1
Q9UMX0	29979	UBQLN1	0	0	0	0	1	1
Q9UNK0	9482	STX8	0	0	0	0	6	3
Q9UNL2	6747	SSR3	0	0	0	0	4	4
Q9UQR0	10389	SCML2	0	0	4	0	1	1
Q9Y237	5303	PIN4	0	0	0	0	1	2
Q9Y265	8607	RUVBL1	0	0	6	0	1	3
Q9Y281	1073	CFL2	0	0	4	0	2	1
Q9Y2G8	23341	DNAJC16	0	0	0	0	1	1
Q9Y2H6	22862	FNDC3A	0	0	0	0	4	7
Q9Y2U8	23592	LEMD3	0	0	0	0	7	6
Q9Y320	51075	TMX2	0	0	0	0	2	3
Q9Y394	51635	DHRS7	0	0	0	0	13	7
Q9Y3P4	25807	RHBDD3	0	0	0	0	1	1
Q9Y450	10767	HBS1L	0	0	0	0	3	5
Q9Y4K4	11183	MAP4K5	0	0	0	0	2	1
Q9Y4P3	26608	TBL2	0	0	0	0	2	2
Q9Y570	51400	PPME1	0	0	0	0	1	1
Q9Y5W8	23161	SNX13	0	0	0	0	1	1
Q9Y5Z7	29915	HCFC2	0	0	1	0	1	1
Q9Y617	29968	PSAT1	0	0	0	1	1	2
Q9Y678	22820	COPG1	0	0	0	0	3	2
Q9Y679	550	AUP1	0	0	0	0	10	5
Q9Y6E0	8428	STK24	0	0	0	0	1	1

Q9Y6X4	26049	FAM169A	0	0	0	0	10	8
Q9Y6Y8	11196	SEC23IP	0	0	0	0	1	4

Appendix D. Summary of topology and TM information of proteins labeled by MCS-ID.

				# PSM							
UniProt	Entrez ID	Gene Name	UniProt-labeled site	MAM normal #1	MAM normal #2	EGFP normal #1	EGFP normal #2	MAM star #1	MAM star #2	EGFP star #1	EGFP star#2
P28288	5825	ABCD3	P28288-416	3	4	0	0	7	4	2	0
O75915	10550	ARL6IP5	O75915-185	3	2	0	0	3	2	0	0
P06576	506	ATP5B	P06576-264	0	1	0	0	1	1	0	0
Q07812	581	BAX	Q07812-21	3	3	0	0	1	4	0	0
Q9BXK5	23786	BCL2L13	Q9BXK5-412	2	1	0	0	1	0	0	0
O15155	10282	BET1	O15155-47	5	5	0	0	8	7	0	0
O15155	10282	BET1	O15155-42	0	0	0	0	1	1	0	0
Q9BWL3	25912	C1orf43	Q9BWL3-73	0	2	0	0	1	2	0	0
Q9BWL3	25912	C1orf43	Q9BWL3-105	2	2	0	0	1	2	0	0
P00918	760	CA2	P00918-212	1	1	0	2	1	2	1	0
Q96A33	57003	CCDC47	Q96A33-419	3	3	0	0	3	3	0	0
Q5VV42	54901	CDKAL1	Q5VV42-65	3	1	0	0	2	2	2	0
Q96S66	23155	CLCC1	Q96S66-437	1	2	0	1	1	3	0	0
Q96S66	23155	CLCC1	Q96S66-414	1	1	0	0	1	1	0	0
P46109	1399	CRKL	P46109-89	1	4	0	8	4	5	7	0
P00167	1528	CYB5A	P00167-33	2	2	0	0	2	2	0	0
O43169	80777	CYB5B	O43169-88	2	3	0	0	3	2	0	0
Q96HY6	65992	DDRGK1	Q96HY6-267	1	1	0	0	1	2	0	0
Q96HY6	65992	DDRGK1	Q96HY6-227	2	2	0	0	2	2	0	0
Q9UBM7	1717	DHCR7	Q9UBM7-13	2	2	0	0	2	1	0	0
Q9Y394	51635	DHRS7	Q9Y394-332	2	1	0	0	2	3	0	0
P50402	2010	EMD	P50402-88	6	9	0	1	9	7	1	0
P50402	2010	EMD	P50402-79	3	3	0	1	3	4	1	0
P50402	2010	EMD	P50402-37	0	3	0	0	3	3	0	0
Q9NVH0	55218	EXD2	Q9NVH0-221	1	3	0	0	2	2	0	0
Q8NAN2	374986	FAM73A	Q8NAN2-118	1	1	0	0	0	1	0	0
Q14318	23770	FKBP8	Q14318-271	4	3	4	0	3	1	0	4

Q9BWH2	65991	FUNDC2	Q9BWH2-150	6	6	0	0	5	6	0	0
Q9BWH2	65991	FUNDC2	Q9BWH2-35	1	1	0	0	0	0	0	0
Q8TB36	54332	GDAP1	Q8TB36-188	2	1	0	0	2	2	0	0
P30519	3163	HMOX2	P30519-259	1	0	0	0	1	1	0	0
Q32P51	144983	HNRNPA1L2	Q32P51-130	1	1	0	0	1	0	0	0
P14625	7184	HSP90B1	P14625-663	2	1	0	0	0	0	0	0
P54652	3306	HSPA2	P54652-510	5	3	0	0	4	3	0	0
P54652	3306	HSPA2	P54652-26	0	0	0	0	1	1	0	0
P05556	3688	ITGB1	P05556-784	2	2	0	0	0	0	0	0
Q14739	3930	LBR	Q14739-190	3	3	0	1	4	3	1	0
Q14739	3930	LBR	Q14739-123	4	3	0	0	4	4	2	0
Q9C0E8	80856	LNP	Q9C0E8-11	0	1	0	0	2	1	0	0
Q9H089	55341	LSG1	Q9H089-594	0	0	0	0	1	1	0	0
Q969Z3	54996	MARC2	Q969Z3-294	6	8	0	0	6	8	0	0
Q7Z434	57506	MAVS	Q7Z434-311	1	1	0	0	1	1	0	0
Q7Z434	57506	MAVS	Q7Z434-348	1	2	0	1	0	1	0	0
Q7Z434	57506	MAVS	Q7Z434-362	2	1	0	0	0	0	0	0
Q07820	4170	MCL1	Q07820-136	1	1	0	0	2	0	0	0
Q9GZY8	56947	MFF	Q9GZY8-114	0	0	0	0	1	1	0	0
Q9GZY8	56947	MFF	Q9GZY8-109	0	0	0	0	1	1	0	0
Q9UH92	6945	MLX	Q9UH92-209	1	0	0	0	1	1	0	0
Q8N4V1	93380	MMGT1	Q8N4V1-122	4	3	0	0	6	3	0	0
Q86UE4	92140	MTDH	Q86UE4-491	1	1	0	0	1	1	1	0
Q5HYI7	345778	MTX3	Q5HYI7-269	1	1	0	0	2	2	0	0
Q5HYI7	345778	MTX3	Q5HYI7-262	1	0	0	0	2	1	0	0
Q15843	4738	NEDD8	Q15843-11	0	0	0	1	1	1	1	0
Q9NX40	54940	OCIAD1	Q9NX40-195	3	3	0	0	4	3	0	0
Q9NX40	54940	OCIAD1	Q9NX40-193	1	2	0	0	1	1	0	0
P07737	5216	PFN1	P07737-38	0	1	0	1	1	2	1	0
O00264	10857	PGRMC1	O00264-96	3	2	0	0	2	2	0	0
Q99640	9088	PKMYT1	Q99640-58	3	3	0	0	3	0	0	0
Q9HCU5	10113	PREB	Q9HCU5-38	2	1	0	0	1	3	0	0

P53801	754	PTTG1IP	P53801-169	1	1	0	1	1	1	0	0
P20340	5870	RAB6A	P20340-53	1	1	0	0	0	0	0	0
Q5HYI8	285282	RABL3	Q5HYI8-231	4	3	0	1	3	3	0	0
Q99942	6048	RNF5	Q99942-75	1	0	0	0	1	1	0	0
O75396	9554	SEC22B	O75396-169	1	3	0	0	4	2	0	0
Q9Y6X1	27230	SERP1	Q9Y6X1-26	1	1	0	0	1	0	0	0
Q96EX1	113444	SMIM12	Q96EX1-73	2	2	0	0	2	1	0	0
Q96E16	114926	SMIM19	Q96E16-74	2	3	0	0	3	4	0	0
O95721	9342	SNAP29	O95721-240	1	1	0	0	1	1	1	0
O95721	9342	SNAP29	O95721-217	3	2	0	0	2	2	0	0
O95721	9342	SNAP29	O95721-201	3	1	1	0	1	4	0	1
Q15005	9789	SPCS2	Q15005-195	1	1	0	0	2	1	0	0
Q9UHB9	6730	SRP68	Q9UHB9-277	1	1	0	0	1	1	0	0
Q9Y5M8	58477	SRPRB	Q9Y5M8-227	1	2	0	0	2	2	0	0
P43307	6745	SSR1	P43307-266	1	2	0	0	4	1	0	0
Q13190	6811	STX5	Q13190-82	0	1	0	0	1	1	0	0
Q13190	6811	STX5	Q13190-241	0	2	0	0	1	1	0	0
P57105	55333	SYNJ2BP	P57105-74	0	0	0	0	1	1	0	0
Q9Y4P3	26608	TBL2	Q9Y4P3-120	2	0	0	0	1	1	0	0
Q9Y2W6	11022	TDRKH	Q9Y2W6-65	1	1	0	0	1	1	0	0
Q9Y6I9	51368	TEX264	Q9Y6I9-300	4	4	0	0	5	5	0	0
Q8N511	147007	TMEM199	Q8N511-107	6	6	0	1	9	9	1	0
Q6NUQ4	54867	TMEM214	Q6NUQ4-46	1	0	0	0	2	1	0	0
Q96A57	29058	TMEM230	Q96A57-16	4	4	0	1	6	4	0	0
Q9P0T7	252839	TMEM9	Q9P0T7-165	2	2	0	0	2	2	0	0
Q9NQ34	56674	TMEM9B	Q9NQ34-171	3	3	0	0	0	2	0	0
P42167	7112	TMPO	P42167-393	2	3	0	0	2	3	0	0
P42167	7112	TMPO	P42167-368	1	0	0	0	1	2	0	0
P42167	7112	TMPO	P42167-334	1	1	0	1	1	1	1	0
P42167	7112	TMPO	P42167-303	2	2	0	0	2	2	3	0
P42167	7112	TMPO	P42167-239	1	0	0	0	2	1	0	0
Q9H3N1	81542	TMX1	Q9H3N1-259	7	4	0	0	4	6	0	0

Q15388	9804	TOMM20	Q15388-68	0	2	0	0	1	1	0	0
Q15388	9804	TOMM20	Q15388-61	4	3	0	0	3	3	0	0
Q15388	9804	TOMM20	Q15388-56	5	2	0	0	3	2	0	0
Q9NS69	56993	TOMM22	Q9NS69-141	0	1	0	0	1	1	0	0
Q8N4H5	401505	TOMM5	Q8N4H5-10	7	6	0	0	5	5	0	0
Q5JTV8	26092	TOR1AIP1	Q5JTV8-308	1	0	0	0	1	3	0	0
O14683	9537	TP53I11	O14683-26	0	3	0	1	4	2	0	0
Q9Y385	51465	UBE2J1	Q9Y385-8	3	4	0	1	1	3	1	0
Q92890	7353	UFD1L	Q92890-267	1	0	1	0	1	1	0	1
Q9NZ43	55850	USE1	Q9NZ43-184	1	1	0	0	1	1	0	0
Q70CQ3	84749	USP30	Q70CQ3-372	0	1	0	0	1	2	0	0
Q8TAA9	81839	VANGL1	Q8TAA9-310	0	1	0	1	1	1	1	0
O95292	9217	VAPB	O95292-155	2	2	0	0	1	1	0	0
O15498	10652	YKT6	O15498-150	8	5	0	1	7	8	1	0

Entrez ID	Gene Name	UniProt-labeled site	TM	Topology before correction	Correction notes for TM and Topology
56993	TOMM22	Q9NS69-141	TRANSMEM 84 103 Helical. {ECO:0000255}.	TOPO_DOM 2 83 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 104 142 Mitochondrial intermembrane. {ECO:0000255}.	TOPO_DOM 2 83 Mitochondrial intermembrane. {ECO:0000255}.; TOPO_DOM 104 142 Cytoplasmic. {ECO:0000255}.
26092	TOR1AIP1	Q5JTV8-308	TRANSMEM 339 355 Helical. {ECO:0000255}.	TOPO_DOM 1 338 Nuclear. {ECO:0000255}.; TOPO_DOM 356 583 Perinuclear space. {ECO:0000255}.	TOPO_DOM 1 338 Perinuclear space. {ECO:0000255}.; TOPO_DOM 356 583 Nuclear. {ECO:0000255}.
5825	ABCD3	P28288-416	TRANSMEM 84 104 Helical. {ECO:0000255|PROSITE-ProRule:PRU00441}.; TRANSMEM 126 146 Helical. {ECO:0000255|PROSITE-ProRule:PRU00441}.; TRANSMEM 224 244 Helical. {ECO:0000255|PROSITE-ProRule:PRU00441}.; TRANSMEM 313 333 Helical.	0	TOPO_DOM 1 83 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 105 125 Lumenal. {ECO:0000255}.; TOPO_DOM 147 223 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 245 312 Lumenal. {ECO:0000255}.; TOPO_DOM 334 659 Cytoplasmic. {ECO:0000255}.

581	BAX	Q07812-21	{ECO:0000255|PROSITE-ProRule:PRU00441}. TRANSMEM 172 192 Helical. {ECO:0000255}.	0	TOPO_DOM 1 171 Cytoplasmic. {ECO:0000255}.
23786	BCL2L13	Q9BXK5-412	TRANSMEM 460 480 Helical. {ECO:0000255}.	0	TOPO_DOM 1 459 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 481 485 Mitochondrial intermembrane. {ECO:0000255}.
25912	C1orf43	Q9BWL3-73	TRANSMEM 11 31 Helical. {ECO:0000255}.	0	TOPO_DOM 1 10 Extracellular. {ECO:0000255}.; TOPO_DOM 32 253 Cytoplasmic. {ECO:0000255}.
25912	C1orf43	Q9BWL3-105	TRANSMEM 11 31 Helical. {ECO:0000255}.	0	TOPO_DOM 1 10 Extracellular. {ECO:0000255}.; TOPO_DOM 32 253 Cytoplasmic. {ECO:0000255}.
57003	CCDC47	Q96A33-419	TRANSMEM 136 155 Helical. {ECO:0000255}.	0	TOPO_DOM 1 135 Lumenal. {ECO:0000255}.; TOPO_DOM 156 483 Cytoplasmic. {ECO:0000255}.
54901	CDKAL1	Q5VV42-65	TRANSMEM 556 578 Helical. {ECO:0000255}.	0	TOPO_DOM 1 555 Cytoplasmic. {ECO:0000255}.
23155	CLCC1	Q96S66-437	TRANSMEM 185 205 Helical. {ECO:0000255}.; TRANSMEM 217 237 Helical. {ECO:0000255}.; TRANSMEM 330 350 Helical. {ECO:0000255}.	0	TOPO_DOM 1 184 Lumenal. {ECO:0000255}.; TOPO_DOM 206 216 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 238 329 Lumenal. {ECO:0000255}.; TOPO_DOM 351 551 Cytoplasmic. {ECO:0000255}.
23155	CLCC1	Q96S66-414	TRANSMEM 185 205 Helical. {ECO:0000255}.; TRANSMEM 217 237 Helical. {ECO:0000255}.; TRANSMEM 330 350 Helical. {ECO:0000255}.	0	TOPO_DOM 1 184 Lumenal. {ECO:0000255}.; TOPO_DOM 206 216 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 238 329 Lumenal. {ECO:0000255}.; TOPO_DOM 351 551 Cytoplasmic. {ECO:0000255}.
1528	CYB5A	P00167-33	TRANSMEM 109 131 Helical. {ECO:0000255}.	0	TOPO_DOM 1 108 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 132 134 Lumenal. {ECO:0000255}.
80777	CYB5B	O43169-88	TRANSMEM 119 136 Helical. {ECO:0000255}.	0	TOPO_DOM 1 118 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 137 146 Mitochondrial intermembrane. {ECO:0000255}.
1717	DHCR7	Q9UBM7-13	TRANSMEM 40 60 Helical. {ECO:0000255}.; TRANSMEM 154 174 Helical. {ECO:0000255}.; TRANSMEM 177 197 Helical. {ECO:0000255}.; TRANSMEM 266 286 Helical. {ECO:0000255}.; TRANSMEM 306 326 Helical. {ECO:0000255}.; TRANSMEM 331 351 Helical.	0	TOPO_DOM 1 39 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 61 153 Lumenal. {ECO:0000255}.; TOPO_DOM 175 176 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 198 265 Lumenal. {ECO:0000255}.; TOPO_DOM 287 305 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 327 330 Lumenal. {ECO:0000255}.; TOPO_DOM 352 419 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 441 475 Lumenal. {ECO:0000255}.

			{ECO:0000255}.; TRANSMEM 420 440 Helical. {ECO:0000255}.		
2010	EMD	P50402-88	TRANSMEM 223 243 Helical. {ECO:0000255}.	0	TOPO_DOM 1 222 Cytoplasmic, Perinuclear space {ECO:0000255}.; TOPO_DOM 244 254 Lumenal, Nuclear {ECO:0000255}.
2010	EMD	P50402-79	TRANSMEM 223 243 Helical. {ECO:0000255}.	0	TOPO_DOM 1 222 Cytoplasmic, Perinuclear space {ECO:0000255}.; TOPO_DOM 244 254 Lumenal, Nuclear {ECO:0000255}.
2010	EMD	P50402-37	TRANSMEM 223 243 Helical. {ECO:0000255}.	0	TOPO_DOM 1 222 Cytoplasmic, Perinuclear space {ECO:0000255}.; TOPO_DOM 244 254 Lumenal, Nuclear {ECO:0000255}.
374986	FAM73A	Q8NAN2-118	TRANSMEM 70 90 Helical. {ECO:0000255}.	0	TOPO_DOM 1 69 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 91 632 Mitochondrial intermembrane. {ECO:0000255}.
23770	FKBP8	Q14318-271	TRANSMEM 390 410 Helical. {ECO:0000255}.	0	TOPO_DOM 1 289 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 410 412 Mitochondrial intermembrane. {ECO:0000255}.
54332	GDAP1	Q8TB36-188	TRANSMEM 292 312 Helical. {ECO:0000255}.; TRANSMEM 320 340 Helical. {ECO:0000255}.	0	TOPO_DOM 1 291 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 313 319 Mitochondrial intermembrane. {ECO:0000255}.; TOPO_DOM 341 358 Cytoplasmic. {ECO:0000255}.
4170	MCL1	Q07820-136	TRANSMEM 328 348 Helical. {ECO:0000255}.	0	TOPO_DOM 1 327 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 349 350 Mitochondrial intermembrane. {ECO:0000255}.
6048	RNF5	Q99942-75	TRANSMEM 118 138 Helical. {ECO:0000255}.; TRANSMEM 160 180 Helical. {ECO:0000255}.	0	TOPO_DOM 1 117 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 139 159 Lumenal. {ECO:0000255}.
113444	SMIM12	Q96EX1-73	TRANSMEM 15 34 Helical. {ECO:0000255}.	0	TOPO_DOM 1 14 Mitochondrial intermembrane. {ECO:0000255}.; TOPO_DOM 35 92 Cytoplasmic. {ECO:0000255}.
114926	SMIM19	Q96E16-74	TRANSMEM 25 43 Helical. {ECO:0000255}.	0	TOPO_DOM 1 24 Extracellular. {ECO:0000255}.; TOPO_DOM 44 107 Cytoplasmic. {ECO:0000255}.
58477	SRPRB	Q9Y5M8-227	TRANSMEM 37 57 Helical. {ECO:0000255}.	0	TOPO_DOM 1 36 Lumenal. {ECO:0000255}.; TOPO_DOM 58 271 Cytoplasmic. {ECO:0000255}.
147007	TMEM199	Q8N511-107	TRANSMEM 146 166 Helical. {ECO:0000255}.; TRANSMEM 179 199 Helical. {ECO:0000255}.	0	TOPO_DOM 1 145 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 167 178 Lumenal. {ECO:0000255}.; TOPO_DOM 200 208 Cytoplasmic. {ECO:0000255}.
54867	TMEM214	Q6NUQ4-46	TRANSMEM 480 500 Helical. {ECO:0000255}.; TRANSMEM 616 636 Helical. {ECO:0000255}.	0	TOPO_DOM 1 479 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 501 615 Lumenal. {ECO:0000255}.; TOPO_DOM 637 689 Cytoplasmic. {ECO:0000255}.
29058	TMEM230	Q96A57-16	TRANSMEM 46 66 Helical.	0	TOPO_DOM 1 45 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 67

			{ECO:0000255}.; TRANSMEM 79 99 Helical. {ECO:0000255}.			78 Lumenal. {ECO:0000255}.; TOPO_DOM 100 120 Cytoplasmic. {ECO:0000255}.
56674	TMEM9B	Q9NQ34-171	TRANSMEM 105 125 Helical. {ECO:0000255}.		0	TOPO_DOM 1 104 Lumenal. {ECO:0000255}.; TOPO_DOM 126 198 Cytoplasmic. {ECO:0000255}.
7112	TMPO	P42167-393	TRANSMEM 411 434 Helical; Signal-anchor for type II membrane protein. {ECO:0000255}.	TOPO_DOM 435 454 Lumenal. {ECO:0000255}.		TOPO_DOM 1 410 Perinuclear space. {ECO:0000255}.; TOPO_DOM 435 454 Lumenal. {ECO:0000255}.
7112	TMPO	P42167-368	TRANSMEM 411 434 Helical; Signal-anchor for type II membrane protein. {ECO:0000255}.	TOPO_DOM 435 454 Lumenal. {ECO:0000255}.		TOPO_DOM 1 410 Perinuclear space. {ECO:0000255}.; TOPO_DOM 435 454 Lumenal. {ECO:0000255}.
7112	TMPO	P42167-334	TRANSMEM 411 434 Helical; Signal-anchor for type II membrane protein. {ECO:0000255}.	TOPO_DOM 435 454 Lumenal. {ECO:0000255}.		TOPO_DOM 1 410 Perinuclear space. {ECO:0000255}.; TOPO_DOM 435 454 Lumenal. {ECO:0000255}.
7112	TMPO	P42167-303	TRANSMEM 411 434 Helical; Signal-anchor for type II membrane protein. {ECO:0000255}.	TOPO_DOM 435 454 Lumenal. {ECO:0000255}.		TOPO_DOM 1 410 Perinuclear space. {ECO:0000255}.; TOPO_DOM 435 454 Lumenal. {ECO:0000255}.
7112	TMPO	P42167-239	TRANSMEM 411 434 Helical; Signal-anchor for type II membrane protein. {ECO:0000255}.	TOPO_DOM 435 454 Lumenal. {ECO:0000255}.		TOPO_DOM 1 410 Perinuclear space. {ECO:0000255}.; TOPO_DOM 435 454 Lumenal. {ECO:0000255}.
401505	TOMM5	Q8N4H5-10	TRANSMEM 27 45 Helical. {ECO:0000255}.		0	TOPO_DOM 1 26 Cytoplasmic. {ECO:0000255}.; TOPO_DOM 46 51 Mitochondrial intermembrane. {ECO:0000255}.

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